GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: December 22, 2002, 07:41:51 ; Search time 2776 Seconds
(without alignments)
13817.543 Million cell updates/sec

Title: US-09-964-994-1
Perfect score: 1318
Sequence: 1 cagtttcttcatctgtaaca.....aaaaaaaaaaaaaaaaaaaa 1318

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
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38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		1318	100.0	1318	6	AX300012	AX300012 Sequence
2		1282.6	97.3	2859	9	AY040567	AY040567 Homo sapi
3		1280.4	97.1	1351	9	HSA313162	AJ313162 Homo sapi
4		1094.4	83.0	2367	6	AX469514	AX469514 Sequence
5		1080.6	82.0	2763	9	AY040566	AY040566 Homo sapi
6		1078.4	81.8	1255	6	AX399654	AX399654 Sequence
7		1078.4	81.8	1255	9	HSA313161	AJ313161 Homo sapi
8		1078	81.8	1618	9	AY044429	AY044429 Homo sapi
9		910	69.0	2271	6	AX469509	AX469509 Sequence
10		831.6	63.1	2149	6	AX151700	AX151700 Sequence
11		831.6	63.1	2149	6	AX179609	AX179609 Sequence
12		805.2	61.1	810	6	AX399656	AX399656 Sequence
13		730.6	55.4	2593	9	AY040568	AY040568 Homo sapi
14		669	50.8	775	9	HSA297262	AJ297262 Homo sapi
15		588.4	44.6	696	6	AX193705	AX193705 Sequence
16		449.2	34.1	750	6	AX193682	AX193682 Sequence
17		449.2	34.1	750	6	AX399652	AX399652 Sequence
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19		404.4	30.7	124324	2	AL158138	AL158138 Homo sapi
20		404.4	30.7	131227	2	AL136098	AL136098 Homo sapi
21		398.2	30.2	693	6	AX151702	AX151702 Sequence
22		398.2	30.2	693	6	AX193707	AX193707 Sequence
23		319.6	24.2	747	6	AX193684	AX193684 Sequence
24		269.8	20.5	526	6	AX193708	AX193708 Sequence
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32	c	68.8	5.2	124820	2	AC117073	AC117073 Dictyoste
33	c	68.6	5.2	105470	2	AC116306	AC116306 Dictyoste
34	c	67.2	5.1	97683	2	AC116548	AC116548 Dictyoste
35		67	5.1	1720	6	AX180193	AX180193 Sequence
36		67	5.1	1720	6	AX180693	AX180693 Sequence
37		67	5.1	1720	6	AX406502	AX406502 Sequence
38		67	5.1	1750	6	AX376330	AX376330 Sequence
39		67	5.1	1750	6	AX464054	AX464054 Sequence
40		67	5.1	1801	6	AX180163	AX180163 Sequence
41		67	5.1	1801	6	AX180663	AX180663 Sequence
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43		67	5.1	3485	9	AF184971	AF184971 Homo sapi
44		67	5.1	3516	6	AX180151	AX180151 Sequence
45		67	5.1	3516	6	AX180651	AX180651 Sequence

ALIGNMENTS

RESULT 1
AX300012
LOCUS AX300012 1318 bp DNA linear PAT 26-NOV-2001
DEFINITION Sequence 17 from Patent WO0166740.
ACCESSION AX300012
VERSION AX300012.1 GI:17129481
KEYWORDS .
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Eaton,D.L., Fong,S., Goddard,A., Godowski,P.J., Grimaldi,C.J.,
Gurney,A.L., Tumas,D., Watanabe,C.K., Wood,W.I. and Zhang,Z.
TITLE Compositions and methods for the treatment of immune related

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          diseases
  JOURNAL Patent: WO 0166740-A 17 13-SEP-2001;
          Genentech, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .1318
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BASE COUNT      451 a    251 c    259 g    357 t
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Query Match 100.0%; Score 1318; DB 6; Length 1318;
Best Local Similarity 100.0%; Pred. No. 9.8e-274;
Matches 1318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy     841 CTATACCGAGTTTTTATAATTAACAATTCACTAGAAAAGGAGCAAAAGGTTTATGAAGGG 900
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LOCUS       AY040567                2859 bp    mRNA    linear   PRI 19-AUG-2001
DEFINITION  Homo sapiens interleukin 22-binding protein CRF2-10L (IL22BP) mRNA,
            complete cds, alternatively spliced.
ACCESSION   AY040567
VERSION     AY040567.1  GI:15212827
KEYWORDS    .
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2859)
  AUTHORS   Kotenko,S.V., Izotova,L.S., Mirochnitchenko,O.V., Esterova,E.,
            Dickensheets,H., Donnelly,R.P. and Pestka,S.
  TITLE     Identification, cloning, and characterization of a novel soluble
            receptor that binds IL-22 and neutralizes its activity
  JOURNAL   J. Immunol. 166 (12), 7096-7103 (2001)
  MEDLINE   21286453
   PUBMED   11390454
REFERENCE   2  (bases 1 to 2859)
  AUTHORS   Kotenko,S.V. and Pestka,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-JUN-2001) Molecular Genetics and Microbiology,
            UMDNJ-Robert Wood Johnson Medical School, 675 Hoes Lane,
            Piscataway, NJ 08854-5635, USA
FEATURES             Location/Qualifiers
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BASE COUNT 893 a 504 c 549 g 913 t
ORIGIN

Query Match 97.3%; Score 1282.6; DB 9; Length 2859;
Best Local Similarity 99.7%; Pred. No. 4.1e-266;
Matches 1285; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy      61 GGATTAACAAAGACAAAATATGGGAAAAACATAACATGGCGTCCCATAATTATTAGATCT 120
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Qy     121 TATTATTGACACTAAAATGGCATTAAAATTACCAAAAGGAAGACAGCATCTGTTTCCTCT 180
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RESULT 3
HSA313162
LOCUS HSA313162 1351 bp mRNA linear PRI 21-OCT-2001
DEFINITION Homo sapiens mRNA for soluble cytokine class II receptor, long isoform (CRF2-S1 gene).
ACCESSION AJ313162
VERSION AJ313162.1 GI:16304592
KEYWORDS alternative splicing; CRF2-S1 gene; long isoform; soluble cytokine class II receptor.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1351)
AUTHORS Gruenberg,B.H., Schoenemeyer,A., Weiss,B., Toschi,L., Kunz,S., Wolk,K., Asadullah,K. and Sabat,R.
TITLE A novel, soluble homologue of the human IL-10 receptor with preferential expression in placenta
JOURNAL Genes Immun. 2 (6), 329-334 (2001)
MEDLINE 21518574
PUBMED 11607789
REFERENCE 2 (bases 1 to 1351)
AUTHORS Weiss,B.
TITLE Direct Submission
JOURNAL Submitted (06-JUN-2001) Weiss B., Genomics & Bioinformatics, Schering AG, Muellerstr. 178, Berlin, D-13342, GERMANY
COMMENT Related sequence AJ313161: short isoform.
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Qy     121 TATTATTGACACTAAAATGGCATTAAAATTACCAAAAGGAAGACAGCATCTGTTTCCTCT 180
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Db     187 TATTATTGACACTAAAATGGCATTAAAATTACCAAAAGGAAGACAGCATCTGTTTCCTCT 246

Qy     181 TTGGTCCTGAGCTGGTTAAAAGGAACACTGGTTGCCTGAACAGTCACACTTGCAACCATG 240
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Db     247 TTGGTCCTGAGCTGGTTAAAAGGAACACTGGTTGCCTGAACAGTCACACTTGCAACCATG 306

Qy     241 ATGCCTAAACATTGCTTTCTAGGCTTCCTCATCAGTTTCTTCCTTACTGGTGTAGCAGGA 300
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Db     307 ATGCCTAAACATTGCTTTCTAGGCTTCCTCATCAGTTTCTTCCTTACTGGTGTAGCAGGA 366

Qy     301 ACTCAGTCAACGCATGAGTCTCTGAAGCCTCAGAGGGTACAATTTCAGTCCCGAAATTTT 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     367 ACTCAGTCAACGCATGAGTCTCTGAAGCCTCAGAGGGTACAATTTCAGTCCCGAAATTTT 426

Qy     361 CACAACATTTTGCAATGGCAGCCTGGGAGGGCACTTACTGGCAACAGCAGTGTCTATTTT 420
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Db     427 CACAACATTTTGCAATGGCAGCCTGGGAGGGCACTTACTGGCAACAGCAGTGTCTATTTT 486

Qy     421 GTGCAGTACAAAATCATGTTCTCATGCAGCATGAAAAGCTCTCACCAGAAGCCAAGTGGA 480
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Db     487 GTGCAGTACAAAATCATGTTCTCATGCAGCATGAAAAGCTCTCACCAGAAGCCAAGTGGA 546

Qy     481 TGCTGGCAGCACATTTCTTGTAACTTCCCAGGCTGCAGAACATTGGCTAAATATGGACAG 540
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Qy     541 AGACAATGGAAAAATAAAGAAGACTGTTGGGGTACTCAAGAACTCTCTTGTGACCTTACC 600
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Db     607 AGACAATGGAAAAATAAAGAAGACTGTTGGGGTACTCAAGAACTCTCTTGTGACCTTACC 666

Qy     601 AGTGAAACCTCAGACATACAGGAACCTTATTACGGGAGGGTGAGGGCGGCCTCGGCTGGG 660
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Qy     661 AGCTACTCAGAATGGAGCATGACGCCGCGGTTCACTCCCTGGTGGGAAACAAAAATAGAT 720
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Db     727 AGCTACTCAGAATGGAGCATGACGCCGCGGTTCACTCCCTGGTGGGAAACAAAAATAGAT 786

Qy     721 CCTCCAGTCATGAATATAACCCAAGTCAATGGCTCTTTGTTGGTAATTCTCCATGCTCCA 780
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Db     787 CCTCCAGTCATGAATATAACCCAAGTCAATGGCTCTTTGTTGGTAATTCTCCATGCTCCA 846

Qy     781 AATTTACCATATAGATACCAAAAGGAAAAAAATGTATCTATAGAAGATTACTATGAACTA 840
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Db     847 AATTTACCATATAGATACCAAAAGGAAAAAAATGTATCTATAGAAGATTACTATGAACTA 906

Qy     841 CTATACCGAGTTTTTATAATTAACAATTCACTAGAAAAGGAGCAAAAGGTTTATGAAGGG 900
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Qy     901 GCTCACAGAGCGGTTGAAATTGAAGCTCTAACACCACACTCCAGCTACTGTGTAGTGGCT 960
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Qy     961 GAAATATATCAGCCCATGTTAGACAGAAGAAGTCAGAGAAGTGAAGAGAGATGTGTGGAA 1020
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Db    1027 GAAATATATCAGCCCATGTTAGACAGAAGAAGTCAGAGAAGTGAAGAGAGATGTGTGGAA 1086

Qy    1021 ATTCCATGACTTGTGGAATTTGGCATTCAGCAATGTGGAAATTCTAAAGCTCCCTGAGAA 1080
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Db    1087 ATTCCATGACTTGTGGAATTTGGCATTCAGCAATGTGGAAATTCTAAAGCTCCCTGAGAA 1146

Qy    1081 CAGGATGACTCGTGTTTGAAGGATCTTATTTAAAATTGTTTTTGTATTTTCTTAAAGCAA 1140
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Db    1147 CAGGATGACTCGTGTTTGAAGGATCTTATTTAAAATTGTTTTTGTATTTTCTTAAAGCAA 1206

Qy    1141 TATTCACTGTTACACCTTGGGGACTTCTTTGTTTATCCATTCTTTTATCCTTTATATTTC 1200
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Db    1207 TATTCACTGTTACACCTTGGGGACTTCTTTGTTTACCCATTCTTTTATCCTTTATATTTC 1266

Qy    1201 ATTTGTAAACTATATTTGAACGACATTCCCCCCGAAAAATTGAAATGTAAAGATGAGGCA 1260
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Db    1267 ATTTGTAAACTATATTTGAACGACATTCCCCCCGAAAAATTGAAATGTAAAGATGAGGCA 1326

Qy    1261 GAGAATAAAGTGTTCTATGAAA 1282
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Db    1327 GAGAATAAAGTGTTCTATGAAA 1348
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RESULT 4
AX469514
LOCUS       AX469514                2367 bp    DNA     linear   PAT 16-JUL-2002
DEFINITION  Sequence 10 from Patent WO0224912.
ACCESSION   AX469514
VERSION     AX469514.1  GI:21901798
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Renauld,J.C. and Dumoutier,L.
  TITLE     Isolated nucleic acid molecules which encode a soluble il-tif/il-22
            receptor or binding protein which binds to il-tif/il-22 and uses
            thereof
  JOURNAL   Patent: WO 0224912-A 10 28-MAR-2002;
            LUDWIG INSTITUTE FOR CANCER RESEARCH (US)
FEATURES             Location/Qualifiers
     source          1. .2367
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                     /db_xref="taxon:9606"
BASE COUNT      735 a    425 c    465 g    742 t
ORIGIN

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Qy     230 TTGCAACCATGATGCCTAAACATTGCTTTCTAGGCTTCCTCATCAGTTTCTTCCTTACTG 289
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Qy    290 GTGTAGCAGGAACTCAGTCAACGCATGAGTCTCTGAAGCCTCAGAGGGTACAATTTCAGT 349
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Db    162 GTGTAGCAGGAACTCAGTCAACGCATGAGTCTCTGAAGCCTCAGAGGGTACAATTTCAGT 221

Qy    350 CCCGAAATTTTCACAACATTTTGCAATGGCAGCCTGGGAGGGCACTTACTGGCAACAGCA 409
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Qy    590 GTGACCTTACCAGTGAAACCTCAGACATACAGGAACCTTATTACGGGAGGGTGAGGGCGG 649
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Db    462 GTGACCTTACCAGTGAAACCTCAGACATACAGGAACCTTATTACGGGAGGGTGAGGGCGG 521

Qy    650 CCTCGGCTGGGAGCTACTCAGAATGGAGCATGACGCCGCGGTTCACTCCCTGGTGGGAAA 709
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Db    522 CCTCGGCTGGGAGCTACTCAGAATGGAGCATGACGCCGCGGTTCACTCCCTGGTGGGAAA 581

Qy    710 CAAAAATAGATCCTCCAGTCATGAATATAACCCAAGTCAATGGCTCTTTGTTGGTAATTC 769
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Db    582 CAAAAATAGATCCTCCAGTCATGAATATAACCCAAGTCAATGGCTCTTTGTTGGTAATTC 641

Qy    770 TCCATGCTCCAAATTTACCATATAGATACCAAAAGGAAAAAAATGTATCTATAGAAGATT 829
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Db    642 TCCATGCTCCAAATTTACCATATAGATACCAAAAGGAAAAAAATGTATCTATAGAAGATT 701

Qy    830 ACTATGAACTACTATACCGAGTTTTTATAATTAACAATTCACTAGAAAAGGAGCAAAAGG 889
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Qy    890 TTTATGAAGGGGCTCACAGAGCGGTTGAAATTGAAGCTCTAACACCACACTCCAGCTACT 949
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Db    762 TTTATGAAGGGGCTCACAGAGCGGTTGAAATTGAAGCTCTAACACCACACTCCAGCTACT 821

Qy    950 GTGTAGTGGCTGAAATATATCAGCCCATGTTAGACAGAAGAAGTCAGAGAAGTGAAGAGA 1009
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Db    822 GTGTAGTGGCTGAAATATATCAGCCCATGTTAGACAGAAGAAGTCAGAGAAGTGAAGAGA 881

Qy   1010 GATGTGTGGAAATTCCATGACTTGTGGAATTTGGCATTCAGCAATGTGGAAATTCTAAAG 1069
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Db    942 CTCCCTGAGAACAGGATGACTCGTGTTTGAAGGATCTTATTTAAAATTGTTTTTGTATTT 1001

Qy   1130 TCTTAAAGCAATATTCACTGTTACACCTTGGGGACTTCTTTGTTTATCCATTCTTTTATC 1189
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Qy   1190 CTTTATATTTCATTTGTAAACTATATTTGAACGACATTCCCCCCGAAAAATTGAAATGTA 1249
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Db   1062 CTTTATATTTCATTTGTAAACTATATTTGAACGACATTCCCCCCGAAAAATTGAAATGTA 1121

Qy   1250 AAGATGAGGCAGAGAATAAAGTGTTCTATGAAAAAAAAAA 1289
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Db   1122 AAGATGAGGCAGAGAATAAAGTGTTCTATGAAATTCAGAA 1161
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RESULT 5
AY040566
LOCUS AY040566 2763 bp mRNA linear PRI 19-AUG-2001
DEFINITION Homo sapiens interleukin 22-binding protein CRF2-10 (IL22BP) mRNA, complete cds.
ACCESSION AY040566
VERSION AY040566.1 GI:15212825
KEYWORDS .
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2763)
AUTHORS Kotenko,S.V., Izotova,L.S., Mirochnitchenko,O.V., Esterova,E., Dickensheets,H., Donnelly,R.P. and Pestka,S.
TITLE Identification, cloning, and characterization of a novel soluble receptor that binds IL-22 and neutralizes its activity
JOURNAL J. Immunol. 166 (12), 7096-7103 (2001)
MEDLINE 21286453
PUBMED 11390454
REFERENCE 2 (bases 1 to 2763)
AUTHORS Kotenko,S.V. and Pestka,S.
TITLE Direct Submission
JOURNAL Submitted (15-JUN-2001) Molecular Genetics and Microbiology, UMDNJ-Robert Wood Johnson Medical School, 675 Hoes Lane, Piscataway, NJ 08854-5635, USA
FEATURES Location/Qualifiers
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gene 1. .2763
/gene="IL22BP"
CDS 275. .970
/gene="IL22BP"
/function="neutralizes IL-22 activity by preventing the binding of IL-22 to the functional cell surface IL-22 receptor complex"
/note="CRF class II member 10; soluble receptor; IL-22BP; member of the class II cytokine receptor family"
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VRAASAGSYSEWSMTPRFTPWWETKIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKN
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RSQRSEERCVEIP"
BASE COUNT 866 a 479 c 528 g 890 t
ORIGIN

Query Match 82.0%; Score 1080.6; DB 9; Length 2763;
Best Local Similarity 92.2%; Pred. No. 1.4e-222;
Matches 1189; Conservative 0; Mismatches 4; Indels 96; Gaps 1;

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Qy      1 CAGTTTCTTCATCTGTAACATCAAATGAATAATAATACCAATCTCCTAGACTTCATAAGA 60
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Db     38 CAGTTTCTTCATCTGTAACATCAAATGAATAATAATACCAATCTCCTAGACTTCATAAGA 97

Qy     61 GGATTAACAAAGACAAAATATGGGAAAAACATAACATGGCGTCCCATAATTATTAGATCT 120
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Db     98 GGATTAACAAAGACAAAATATGGGAAAAACATAACATGGCGTCCCATAATTATTAGATCT 157

Qy    121 TATTATTGACACTAAAATGGCATTAAAATTACCAAAAGGAAGACAGCATCTGTTTCCTCT 180
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Db    158 TATTATTGACACTAAAATGGCATTAAAATTACCAAAAGGAAGACAGCATCTGTTTCCTCT 217

Qy    181 TTGGTCCTGAGCTGGTTAAAAGGAACACTGGTTGCCTGAACAGTCACACTTGCAACCATG 240
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Qy    241 ATGCCTAAACATTGCTTTCTAGGCTTCCTCATCAGTTTCTTCCTTACTGGTGTAGCAGGA 300
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Qy    301 ACTCAGTCAACGCATGAGTCTCTGAAGCCTCAGAGGGTACAATTTCAGTCCCGAAATTTT 360
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Db    458 GTGCAGTACAAAAT---------------------------------------------- 471

Qy    481 TGCTGGCAGCACATTTCTTGTAACTTCCCAGGCTGCAGAACATTGGCTAAATATGGACAG 540
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Qy    961 GAAATATATCAGCCCATGTTAGACAGAAGAAGTCAGAGAAGTGAAGAGAGATGTGTGGAA 1020
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Qy   1201 ATTTGTAAACTATATTTGAACGACATTCCCCCCGAAAAATTGAAATGTAAAGATGAGGCA 1260
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Qy   1261 GAGAATAAAGTGTTCTATGAAAAAAAAAA 1289
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Db   1202 GAGAATAAAGTGTTCTATGAAATTCAGAA 1230
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RESULT 6
AX399654
LOCUS AX399654 1255 bp DNA linear PAT 06-JUN-2002
DEFINITION Sequence 3 from Patent EP1191035.

ACCESSION AX399654
VERSION AX399654.1 GI:21335431
KEYWORDS .
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Weiss,B., Sabat,R., Assadullah,K. and Toshi,L.
TITLE Three members of the cytokin-receptor class II family
JOURNAL Patent: EP 1191035-A 3 27-MAR-2002;
SCHERING AKTIENGESELLSCHAFT (DE)
FEATURES Location/Qualifiers
source 1. .1255
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 402 a 251 c 246 g 356 t
ORIGIN

Query Match 81.8%; Score 1078.4; DB 6; Length 1255;
Best Local Similarity 92.4%; Pred. No. 4.1e-222;
Matches 1185; Conservative 0; Mismatches 1; Indels 96; Gaps 1;

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Db    307 ATGCCTAAACATTGCTTTCTAGGCTTCCTCATCAGTTTCTTCCTTACTGGTGTAGCAGGA 366

Qy    301 ACTCAGTCAACGCATGAGTCTCTGAAGCCTCAGAGGGTACAATTTCAGTCCCGAAATTTT 360
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Db    367 ACTCAGTCAACGCATGAGTCTCTGAAGCCTCAGAGGGTACAATTTCAGTCCCGAAATTTT 426

Qy    361 CACAACATTTTGCAATGGCAGCCTGGGAGGGCACTTACTGGCAACAGCAGTGTCTATTTT 420
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Db    427 CACAACATTTTGCAATGGCAGCCTGGGAGGGCACTTACTGGCAACAGCAGTGTCTATTTT 486

Qy    421 GTGCAGTACAAAATCATGTTCTCATGCAGCATGAAAAGCTCTCACCAGAAGCCAAGTGGA 480
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Db    487 GTGCAGTACAAAAT---------------------------------------------- 500

Qy    481 TGCTGGCAGCACATTTCTTGTAACTTCCCAGGCTGCAGAACATTGGCTAAATATGGACAG 540
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Db    501 ----------------------------------------------------ATATGGACAG 510

Qy    541 AGACAATGGAAAAATAAAGAAGACTGTTGGGGTACTCAAGAACTCTCTTGTGACCTTACC 600
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Db    511 AGACAATGGAAAAATAAAGAAGACTGTTGGGGTACTCAAGAACTCTCTTGTGACCTTACC 570

Qy    601 AGTGAAACCTCAGACATACAGGAACCTTATTACGGGAGGGTGAGGGCGGCCTCGGCTGGG 660
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Db    571 AGTGAAACCTCAGACATACAGGAACCTTATTACGGGAGGGTGAGGGCGGCCTCGGCTGGG 630

Qy    661 AGCTACTCAGAATGGAGCATGACGCCGCGGTTCACTCCCTGGTGGGAAACAAAAATAGAT 720
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Db    631 AGCTACTCAGAATGGAGCATGACGCCGCGGTTCACTCCCTGGTGGGAAACAAAAATAGAT 690

Qy    721 CCTCCAGTCATGAATATAACCCAAGTCAATGGCTCTTTGTTGGTAATTCTCCATGCTCCA 780
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Db    691 CCTCCAGTCATGAATATAACCCAAGTCAATGGCTCTTTGTTGGTAATTCTCCATGCTCCA 750

Qy    781 AATTTACCATATAGATACCAAAAGGAAAAAAATGTATCTATAGAAGATTACTATGAACTA 840
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Db    751 AATTTACCATATAGATACCAAAAGGAAAAAAATGTATCTATAGAAGATTACTATGAACTA 810

Qy    841 CTATACCGAGTTTTTATAATTAACAATTCACTAGAAAAGGAGCAAAAGGTTTATGAAGGG 900
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Db    811 CTATACCGAGTTTTTATAATTAACAATTCACTAGAAAAGGAGCAAAAGGTTTATGAAGGG 870

Qy    901 GCTCACAGAGCGGTTGAAATTGAAGCTCTAACACCACACTCCAGCTACTGTGTAGTGGCT 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    871 GCTCACAGAGCGGTTGAAATTGAAGCTCTAACACCACACTCCAGCTACTGTGTAGTGGCT 930

Qy    961 GAAATATATCAGCCCATGTTAGACAGAAGAAGTCAGAGAAGTGAAGAGAGATGTGTGGAA 1020
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Db    931 GAAATATATCAGCCCATGTTAGACAGAAGAAGTCAGAGAAGTGAAGAGAGATGTGTGGAA 990

Qy   1021 ATTCCATGACTTGTGGAATTTGGCATTCAGCAATGTGGAAATTCTAAAGCTCCCTGAGAA 1080
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Db    991 ATTCCATGACTTGTGGAATTTGGCATTCAGCAATGTGGAAATTCTAAAGCTCCCTGAGAA 1050

Qy   1081 CAGGATGACTCGTGTTTGAAGGATCTTATTTAAAATTGTTTTTGTATTTTCTTAAAGCAA 1140
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Db   1051 CAGGATGACTCGTGTTTGAAGGATCTTATTTAAAATTGTTTTTGTATTTTCTTAAAGCAA 1110

Qy   1141 TATTCACTGTTACACCTTGGGGACTTCTTTGTTTATCCATTCTTTTATCCTTTATATTTC 1200
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Qy   1201 ATTTGTAAACTATATTTGAACGACATTCCCCCCGAAAAATTGAAATGTAAAGATGAGGCA 1260
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Db   1171 ATTTGTAAACTATATTTGAACGACATTCCCCCCGAAAAATTGAAATGTAAAGATGAGGCA 1230

Qy   1261 GAGAATAAAGTGTTCTATGAAA 1282
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RESULT 7
HSA313161
LOCUS       HSA313161              1255 bp    mRNA    linear   PRI 21-OCT-2001
DEFINITION  Homo sapiens mRNA for soluble cytokine class II receptor, short
            isoform (CRF2-S1 gene).
ACCESSION   AJ313161
VERSION     AJ313161.1  GI:16304590
KEYWORDS    alternative splicing; CRF2-S1 gene; short isoform; soluble cytokine
            class II receptor.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1255)
  AUTHORS   Gruenberg,B.H., Schoenemeyer,A., Weiss,B., Toschi,L., Kunz,S.,
            Wolk,K., Asadullah,K. and Sabat,R.
  TITLE     A novel, soluble homologue of the human IL-10 receptor with
            preferential expression in placenta
  JOURNAL   Genes Immun. 2 (6), 329-334 (2001)
  MEDLINE   21518574
   PUBMED   11607789
REFERENCE   2  (bases 1 to 1255)
  AUTHORS   Weiss,B.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-JUN-2001) Weiss B., Genomics & Bioinformatics,
            Schering AG, Muellerstr. 178, Berlin, D-13342, GERMANY
COMMENT     Related sequence AJ313162: long isoform.
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                     /dev_stage="adult"
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     CDS             304. .999
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                     /db_xref="GI:16304591"
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                     /gene="CRF2-S1"
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     3'UTR           1000. .1255
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BASE COUNT      402 a    251 c    246 g    356 t
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Query Match 81.8%; Score 1078.4; DB 9; Length 1255;
Best Local Similarity 92.4%; Pred. No. 4.1e-222;
Matches 1185; Conservative 0; Mismatches 1; Indels 96; Gaps 1;

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Qy      1 CAGTTTCTTCATCTGTAACATCAAATGAATAATAATACCAATCTCCTAGACTTCATAAGA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     67 CAGTTTCTTCATCTGTAACATCAAATGAATAATAATACCAATCTCCTAGACTTCATAAGA 126

Qy     61 GGATTAACAAAGACAAAATATGGGAAAAACATAACATGGCGTCCCATAATTATTAGATCT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    127 GGATTAACAAAGACAAAATATGGGAAAAACATAACATGGCGTCCCATAATTATTAGATCT 186

Qy    121 TATTATTGACACTAAAATGGCATTAAAATTACCAAAAGGAAGACAGCATCTGTTTCCTCT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    187 TATTATTGACACTAAAATGGCATTAAAATTACCAAAAGGAAGACAGCATCTGTTTCCTCT 246

Qy    181 TTGGTCCTGAGCTGGTTAAAAGGAACACTGGTTGCCTGAACAGTCACACTTGCAACCATG 240
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Db    247 TTGGTCCTGAGCTGGTTAAAAGGAACACTGGTTGCCTGAACAGTCACACTTGCAACCATG 306

Qy    241 ATGCCTAAACATTGCTTTCTAGGCTTCCTCATCAGTTTCTTCCTTACTGGTGTAGCAGGA 300
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Db    307 ATGCCTAAACATTGCTTTCTAGGCTTCCTCATCAGTTTCTTCCTTACTGGTGTAGCAGGA 366

Qy    301 ACTCAGTCAACGCATGAGTCTCTGAAGCCTCAGAGGGTACAATTTCAGTCCCGAAATTTT 360
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Db    367 ACTCAGTCAACGCATGAGTCTCTGAAGCCTCAGAGGGTACAATTTCAGTCCCGAAATTTT 426

Qy    361 CACAACATTTTGCAATGGCAGCCTGGGAGGGCACTTACTGGCAACAGCAGTGTCTATTTT 420
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Db    427 CACAACATTTTGCAATGGCAGCCTGGGAGGGCACTTACTGGCAACAGCAGTGTCTATTTT 486

Qy    421 GTGCAGTACAAAATCATGTTCTCATGCAGCATGAAAAGCTCTCACCAGAAGCCAAGTGGA 480
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Db    487 GTGCAGTACAAAAT---------------------------------------------- 500

Qy    481 TGCTGGCAGCACATTTCTTGTAACTTCCCAGGCTGCAGAACATTGGCTAAATATGGACAG 540
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Db    501 ----------------------------------------------------ATATGGACAG 510

Qy    541 AGACAATGGAAAAATAAAGAAGACTGTTGGGGTACTCAAGAACTCTCTTGTGACCTTACC 600
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Db    511 AGACAATGGAAAAATAAAGAAGACTGTTGGGGTACTCAAGAACTCTCTTGTGACCTTACC 570
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Qy    601 AGTGAAACCTCAGACATACAGGAACCTTATTACGGGAGGGTGAGGGCGGCCTCGGCTGGG 660
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Db    571 AGTGAAACCTCAGACATACAGGAACCTTATTACGGGAGGGTGAGGGCGGCCTCGGCTGGG 630

Qy    661 AGCTACTCAGAATGGAGCATGACGCCGCGGTTCACTCCCTGGTGGGAAACAAAAATAGAT 720
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Db    631 AGCTACTCAGAATGGAGCATGACGCCGCGGTTCACTCCCTGGTGGGAAACAAAAATAGAT 690

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Qy    841 CTATACCGAGTTTTTATAATTAACAATTCACTAGAAAAGGAGCAAAAGGTTTATGAAGGG 900
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Qy    901 GCTCACAGAGCGGTTGAAATTGAAGCTCTAACACCACACTCCAGCTACTGTGTAGTGGCT 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    871 GCTCACAGAGCGGTTGAAATTGAAGCTCTAACACCACACTCCAGCTACTGTGTAGTGGCT 930

Qy    961 GAAATATATCAGCCCATGTTAGACAGAAGAAGTCAGAGAAGTGAAGAGAGATGTGTGGAA 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    931 GAAATATATCAGCCCATGTTAGACAGAAGAAGTCAGAGAAGTGAAGAGAGATGTGTGGAA 990

Qy   1021 ATTCCATGACTTGTGGAATTTGGCATTCAGCAATGTGGAAATTCTAAAGCTCCCTGAGAA 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    991 ATTCCATGACTTGTGGAATTTGGCATTCAGCAATGTGGAAATTCTAAAGCTCCCTGAGAA 1050

Qy   1081 CAGGATGACTCGTGTTTGAAGGATCTTATTTAAAATTGTTTTTGTATTTTCTTAAAGCAA 1140
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Db   1051 CAGGATGACTCGTGTTTGAAGGATCTTATTTAAAATTGTTTTTGTATTTTCTTAAAGCAA 1110

Qy   1141 TATTCACTGTTACACCTTGGGGACTTCTTTGTTTATCCATTCTTTTATCCTTTATATTTC 1200
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Db   1111 TATTCACTGTTACACCTTGGGGACTTCTTTGTTTACCCATTCTTTTATCCTTTATATTTC 1170

Qy   1201 ATTTGTAAACTATATTTGAACGACATTCCCCCCGAAAAATTGAAATGTAAAGATGAGGCA 1260
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Db   1171 ATTTGTAAACTATATTTGAACGACATTCCCCCCGAAAAATTGAAATGTAAAGATGAGGCA 1230

Qy   1261 GAGAATAAAGTGTTCTATGAAA 1282
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Db   1231 GAGAATAAAGTGTTCTATGAAA 1252
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ULT 8
AY044429

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LOCUS       AY044429                1618 bp    mRNA    linear   PRI 01-SEP-2001
DEFINITION  Homo sapiens class II cytokine receptor (IL22RA2) mRNA, complete
            cds.
ACCESSION   AY044429
VERSION     AY044429.1  GI:15419022
KEYWORDS    .
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1618)
  AUTHORS   Xu,W., Presnell,S.R., Parrish-Novak,J., Kindsvogel,W., Jaspers,S.,
            Chen,Z., Dillon,S.R., Gao,Z., Gilbert,T., Madden,K.,
            Schlutsmeyer,S., Yao,L., Whitmore,T.E., Chandrasekher,Y.,
            Grant,F.J., Maurer,M., Jelinek,L., Storey,H., Brender,T.,
            Hammond,A., Topouzis,S., Clegg,C.H. and Foster,D.C.
  TITLE     A soluble class II cytokine receptor, IL-22RA2, is a naturally
            occurring IL-22 antagonist
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 98 (17), 9511-9516 (2001)
  MEDLINE   21396522
   PUBMED   11481447
REFERENCE   2  (bases 1 to 1618)
  AUTHORS   Xu,W., Presnell,S.R., Parrish-Novak,J., Kindsvogel,W., Jaspers,S.,
            Chen,Z., Dillon,S.R., Gao,Z., Gilbert,T., Madden,K.,
            Schlutsmeyer,S., Yao,L., Whitmore,T.E., Chandrasekher,Y.,
            Grant,F.J., Maurer,M., Jelinek,L., Storey,H., Brender,T.,
            Hammond,A., Topouzis,S., Clegg;C.H. and Foster,D.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-JUL-2001) Bioinformatics, ZymoGenetics, Inc., 1201
            Eastlake Avenue East, Seattle, WA 98102, USA
FEATURES             Location/Qualifiers
     source          1. .1618
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     gene            1. .1618
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BASE COUNT      562 a    277 c    286 g    493 t
ORIGIN
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  Best Local Similarity   92.2%;  Pred. No. 5e-222;
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Db      1 AGTTTCTTCATCTGTAACATCAAATGAATAATAATACCAATCTCCTAGACTTCATAAGAG 60

Qy     62 GATTAACAAAGACAAAATATGGGAAAAACATAACATGGCGTCCCATAATTATTAGATCTT 121
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Qy    122 ATTATTGACACTAAAATGGCATTAAAATTACCAAAAGGAAGACAGCATCTGTTTCCTCTT 181
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Qy    182 TGGTCCTGAGCTGGTTAAAAGGAACACTGGTTGCCTGAACAGTCACACTTGCAACCATGA 241
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Qy    242 TGCCTAAACATTGCTTTCTAGGCTTCCTCATCAGTTTCTTCCTTACTGGTGTAGCAGGAA 301
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Qy    302 CTCAGTCAACGCATGAGTCTCTGAAGCCTCAGAGGGTACAATTTCAGTCCCGAAATTTTC 361
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Qy    362 ACAACATTTTGCAATGGCAGCCTGGGAGGGCACTTACTGGCAACAGCAGTGTCTATTTTG 421
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Qy    422 TGCAGTACAAAATCATGTTCTCATGCAGCATGAAAAGCTCTCACCAGAAGCCAAGTGGAT 481
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Qy    482 GCTGGCAGCACATTTCTTGTAACTTCCCAGGCTGCAGAACATTGGCTAAATATGGACAGA 541
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Qy    542 GACAATGGAAAAATAAAGAAGACTGTTGGGGTACTCAAGAACTCTCTTGTGACCTTACCA 601
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Db    445 GACAATGGAAAAATAAAGAAGACTGTTGGGGTACTCAAGAACTCTCTTGTGACCTTACCA 504

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Qy    662 GCTACTCAGAATGGAGCATGACGCCGCGGTTCACTCCCTGGTGGGAAACAAAAATAGATC 721

Db    565 GCTACTCAGAATGGAGCATGACGCCGCGGTTCACTCCCTGGTGGGAAACAAAAATAGATC 624

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Db    625 CTCCAGTCATGAATATAACCCAAGTCAATGGCTCTTTGTTGGTAATTCTCCATGCTCCAA 684

Qy    782 ATTTACCATATAGATACCAAAAGGAAAAAAAATGTATCTATAGAAGATTACTATGAACTAC 841

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      745 TATACCGAGTTTTTATAATTAACAATTCACTAGAAAAGGAGCAAAAGGTTTATGAAGGGG 804

Qy    902 CTCACAGAGCGGTTGAAATTGAAGCTCTAACACCACACTCCAGCTACTGTGTAGTGGCTG 961

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Db    925 TTCCATGACTTGTGGAATTTGGCATTCAGCAATGTGGAAATTCTAAAGCTCCCTGAGAAC 984

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Db    985 AGGATGACTCGTGTTTGAAGGATCTTATTTAAAATTGTTTTTGTATTTTCTTAAAGCAAT 1044

Qy   1142 ATTCACTGTTACACCTTGGGGACTTCTTTGTTTATCCATTCTTTTATCCTTTATATTTCA 1201

Db   1045 ATTCACTGTTACACCTTGGGGACTTCTTTGTTTATCCATTCTTTTATCCTTTATATTTCA 1104

Qy   1202 TTTGTAAACTATATTTGAACGACATTCCCCCCCGAAAAATTGAAATGTAAAGATGAGGCAG 1261

Db   1105 TTTGTAAACTATATTTGAACGACATTCCCCCCCGAAAAATTGAAATGTAAAGATGAGGCAG 1164

Qy   1262 AGAATAAAGTGTTCTATGAAAAAAAAAA 1289

     1165 AGAATAAAGTGTTCTATGAAATTCAGAA 1192
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RESULT 9
AX469509
LOCUS       AX469509               2271 bp    DNA     linear   PAT 16-JUL-2002
DEFINITION  Sequence 5 from Patent WO0224912.
ACCESSION   AX469509
VERSION     AX469509.1  GI:21901794
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Renauld,J.C. and Dumoutier,L.
  TITLE     Isolated nucleic acid molecules which encode a soluble il-tif/il-22
            receptor or binding protein which binds to il-tif/il-22 and uses
            thereof
  JOURNAL   Patent: WO 0224912-A 5 28-MAR-2002;
            LUDWIG INSTITUTE FOR CANCER RESEARCH (US)
FEATURES             Location/Qualifiers
     source          1. .2271
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT      709 a    400 c    444 g    718 t
ORIGIN
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Query Match 69.0%; Score 910; DB 6; Length 2271;
Best Local Similarity 91.0%; Pred. No. 7.9e-186;
Matches 1019; Conservative 0; Mismatches 5; Indels 96; Gaps 1;

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Qy    170 CTGTTTCCTCTTTGGTCCTGAGCTGGTTAAAAGGAACACTGGTTGCCTGAACAGTCACAC 229

Db     42 CAGTTTCCTCTTTGGTCCTGAGCTGGTTAAAAGGAACACTGGTTGCCTGAACAGTCACAC 101

Qy    230 TTGCAACCATGATGCCTAAACATTGCTTTCTAGGCTTCCTCATCAGTTTCTTCCTTACTG 289

Db    102 TTGCAACCATGATGCCTAAACATTGCTTTCTAGGCTTCCTCATCAGTTTCTTCCTTACTG 161

Qy    290 GTGTAGCAGGAACTCAGTCAACGCATGAGTCTCTGAAGCCTCAGAGGGTACAATTTCAGT 349

Db    162 GTGTAGCAGGAACTCAGTCAACGCATGAGTCTCTGAAGCCTCAGAGGGTACAATTTCAGT 221

Qy    350 CCCGAAATTTTCACAACATTTTGCAATGGCAGCCTGGGAGGGCACTTACTGGCAACAGCA 409

Db    222 CCCGAAATTTTCACAACATTTTGCAATGGCAGCCTGGGAGGGCACTTACTGGCAACAGCA 281

Qy    410 GTGTCTATTTTGTGCAGTACAAAATCATGTTCTCATGCAGCATGAAAAGCTCTCACCAGA 469

Db    282 GTGTCTATTTTGTGCAGTACAAAAT---------------------------------- 306

Qy    470 AGCCAAGTGGATGCTGGCAGCACATTTCTTGTAACTTCCCAGGCTGCAGAACATTGGCTA 529

Db    307 ---------------------------------------------------------- 306

Qy    530 AATATGGACAGAGACAATGGAAAAATAAAGAAGACTGTTGGGGTACTCAAGAACTCTCTT 589

Db    307 -ATATGGACAGAGACAATGGAAAAATAAAGAAGACTGTTGGGGTACTCAAGAACTCTCTT 365

Qy    590 GTGACCTTACCAGTGAAACCTCAGACATACAGGAACCTTATTACGGGAGGGTGAGGGCGG 649

Db    366 GTGACCTTACCAGTGAAACCTCAGACATACAGGAACCTTATTACGGGAGGGTGAGGGCGG 425

Qy    650 CCTCGGCTGGGAGCTACTCAGAATGGAGCATGACGCCGCGGTTCACTCCCTGGTGGGAAA 709

Db    426 CCTCGGCTGGGAGCTACTCAGAATGGAGCATGACGCCGCGGTTCACTCCCTGGTGGGAAA 485

Qy    710 CAAAAATAGATCCTCCAGTCATGAATATAACCCAAGTCAATGGCTCTTTGTTGGTAATTC 769

Db    486 CAAAAATAGATCCTCCAGTCATGAATATAACCCAAGTCAATGGCTCTTTGTTGGTAATTC 545

Qy    770 TCCATGCTCCAAATTTACCATATAGATACCAAAAGGAAAAAAAATGTATCTATAGAAGATT 829

Db    546 TCCATGCTCCAAATTTACCATATAGATACCAAAAGGAAAAAAAATGTATCTATAGAAGATT 605

Qy    830 ACTATGAACTACTATACCGAGTTTTTATAATTAACAATTCACTAGAAAAGGAGCAAAAGG 889

Db    606 ACTATGAACTACTATACCGAGTTTTTATAATTAACAATTCACTAGAAAAGGAGCAAAAGG 665

Qy    890 TTTATGAAGGGGCTCACAGAGCGGTTGAAATTGAAGCTCTAACACCACACTCCAGCTACT 949

Db    666 TTTATGAAGGGGCTCACAGAGCGGTTGAAATTGAAGCTCTAACACCACACTCCAGCTACT 725

Qy    950 GTGTAGTGGCTGAAATATATCAGCCCATGTTAGACAGAAGAAGTCAGAGAAGTGAAGAGA 1009

Db    726 GTGTAGTGGCTGAAATATATCAGCCCATGTTAGACAGAAGAAGTCAGAGAAGTGAAGAGA 785

Qy   1010 GATGTGTGGAAATTCCATGACTTGTGGAATTTGGCATTCAGCAATGTGGAAATTCTAAAG 1069

Db    786 GATGTGTGGAAATTCCATGACTTGTGGAATTTGGCATTCAGCAATGTGGAAATTCTAAAG 845

Qy   1070 CTCCCTGAGAACAGGATGACTCGTGTTTGAAGGATCTTATTTAAAATTGTTTTTGTATTT 1129

Db    846 CTCCCTGAGAACAGGATGACTCGTGTTTGAAGGATCTTATTTAAAATTGTTTTTGTATTT 905

Qy   1130 TCTTAAAGCAATATTCACTGTTACACCTTGGGGACTTCTTTGTTTATCCATTCTTTTATC 1189
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Db    906 TCTTAAAGCAATATTCACTGTTACACCTTGGGGACTTCTTTGTTTATCCATTCTTTTATC 965

Qy   1190 CTTTATATTTCATTTGTAAACTATATTTGAACGACATTCCCCCCGAAAAATTGAAATGTA 1249
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    966 CTTTATATTTCATTTGTAAACTATATTTGAACGACATTCCCCCCGAAAAATTGAAATGTA 1025

Qy   1250 AAGATGAGGCAGAGAATAAAGTGTTCTATGAAAAAAAAAA 1289
          |||||||||||||||||||||||||||||||||    | ||
Db   1026 AAGATGAGGCAGAGAATAAAGTGTTCTATGAAATTCAGAA 1065


RESULT 10
AX151700
LOCUS       AX151700               2149 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 1 from Patent WO0140467.
ACCESSION   AX151700
VERSION     AX151700.1  GI:14533639
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2149)
  AUTHORS   Presnell,S.R., Xu,W., Kindsvogel,W. and Chen,Z.
  TITLE     Human cytokine receptor
  JOURNAL   Patent: WO 0140467-A 1 07-JUN-2001;
            ZymoGenetics, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .2149
                     /organism="Homo sapiens"
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     CDS             1. .696
                     /note="unnamed protein product"
                     /codon_start=1
                     /protein_id="CAC42591.1"
                     /db_xref="GI:14533640"
                     /translation="MMPKHCFLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNI
                     LQWQPGRALTGNSSVYFVQYKIYGQRQWKNKEDCWGTQELSCDLTSETSDIQEPYYGR
                     VRAASAGSYSEWSMTPRFTPWWETKIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKN
                     VSIEDYYELLYRVFIINNSLEKEQKVYEGAHRAVEIEALTPHSSYCVVAEIYQPMLDR
                     RSQRSEERCVEIP"
BASE COUNT      685 a    381 c    421 g    662 t
ORIGIN

  Query Match           63.1%;  Score 831.6;  DB 6;  Length 2149;
  Best Local Similarity 90.4%;  Pred. No. 6.1e-169;
  Matches  951;  Conservative    0;  Mismatches    4;  Indels   97;  Gaps    2;

      238 ATGATGCCTAAACATTGCTTTCTAGGCTTCCTCATCAGTTTCTTCCTTACTGGTGTAGCA 297
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGATGCCTAAACATTGCTTTCTAGGCTTCCTCATCAGTTTCTTCCTTACTGGTGTAGCA 60

Qy    298 GGAACTCAGTCAACGCATGAGTCTCTGAAGCCTCAGAGGGTACAATTTCAGTCCCGAAAT 357
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GGAACTCAGTCAACGCATGAGTCTCTGAAGCCTCAGAGGGTACAATTTCAGTCCCGAAAT 120

Qy    358 TTTCACAACATTTTGCAATGGCAGCCTGGGAGGGCACTTACTGGCAACAGCAGTGTCTAT 417
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Db    121 TTTCACAACATTTTGCAATGGCAGCCTGGGAGGGCACTTACTGGCAACAGCAGTGTCTAT 180

Qy    418 TTTGTGCAGTACAAAATCATGTTCTCATGCAGCATGAAAAGCTCTCACCAGAAGCCAAGT 477
          ||||||||||||||||
Db    181 TTTGTGCAGTACAAAAT----------------------------------------------- 197

Qy    478 GGATGCTGGCAGCACATTTCTTGTAACTTCCCAGGCTGCAGAACATTGGCTAAATATGGA 537
                                                                |||||||
Db    198 ----------------------------------------------------ATATGGA 204

Qy    538 CAGAGACAATGGAAAAATAAAGAAGACTGTTGGGGTACTCAAGAACTCTCTTGTGACCTT 597
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    205 CAGAGACAATGGAAAAATAAAGAAGACTGTTGGGGTACTCAAGAACTCTCTTGTGACCTT 264

Qy    598 ACCAGTGAAACCTCAGACATACAGGAACCTTATTACGGGAGGGTGAGGGCGGCCTCGGCT 657
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Db    265 ACCAGTGAAACCTCAGACATACAGGAACCTTATTACGGGAGGGTGAGGGCGGCCTCGGCT 324

Qy    658 GGGAGCTACTCAGAATGGAGCATGACGCCGCGGTTCACTCCCTGGTGGGAAACAAAAATA 717
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    325 GGGAGCTACTCAGAATGGAGCATGACGCCGCGGTTCACTCCCTGGTGGGAAACAAAAATA 384

Qy    718 GATCCTCCAGTCATGAATATAACCCAAGTCAATGGCTCTTTGTTGGTAATTCTCCATGCT 777
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    385 GATCCTCCAGTCATGAATATAACCCAAGTCAATGGCTCTTTGTTGGTAATTCTCCATGCT 444

Qy    778 CCAAATTTACCATATAGATACCAAAAGGAAAAAAATGTATCTATAGAAGATTACTATGAA 837
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    445 CCAAATTTACCATATAGATACCAAAAGGAAAAAAATGTATCTATAGAAGATTACTATGAA 504

Qy    838 CTACTATACCGAGTTTTTATAATTAACAATTCACTAGAAAAGGAGCAAAAGGTTTATGAA 897
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Db    505 CTACTATACCGAGTTTTTATAATTAACAATTCACTAGAAAAGGAGCAAAAGGTTTATGAA 564

Qy    898 GGGGCTCACAGAGCGGTTGAAATTGAAGCTCTAACACCACACTCCAGCTACTGTGTAGTG 957
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    565 GGGGCTCACAGAGCGGTTGAAATTGAAGCTCTAACACCACACTCCAGCTACTGTGTAGTG 624

Qy    958 GCTGAAATATATCAGCCCATGTTAGACAGAAGAAGTCAGAGAAGTGAAGAGAGATGTGTG 1017
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    625 GCTGAAATATATCAGCCCATGTTAGACAGAAGAAGTCAGAGAAGTGAAGAGAGATGTGTG 684

Qy   1018 GAAATTCCATGACTTGTGGAATTTGGCATTCAGCAATGTGGAAATTCTAAAGCTCCCTGA 1077
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Db    685 GAAATTCCATGACTTGTGGAATTTGGCATTCAGCAATGTGGAAATTCTAAAGCTCCCTGA 744

Qy   1078 GAACAGGATGACTCGTGTTTGAAGGATCTTATTTAAAATTGTTTTTGTATTTTCTTAAAG 1137
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    745 GAACAGGATGACTCGTGTTTGAAGGATCTTATTTAAAATTGTTTTTGTATTTTCTTAAAG 804

Qy   1138 CAATATTCACTGTTACACCTTGGGGACTTCTTTGTTTATCCATTCTTTTATCCTTTATAT 1197
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    805 CAATATTCACTGTTACACCTTGGGGACTTCTTTGTTTATCCATTCTTTTATCCTTTATAT 864

Qy   1198 TTCATTTGTAAACTATATTTGAACGACATTCCCCCCGAAAAATTGAAATGTAAAGATGAG 1257
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    865 TTCATTT-TAAACTATATTTGAACGACATTCCCCCCGAAAAATTGAAATGTAAAGATGAG 923

Qy   1258 GCAGAGAATAAAGTGTTCTATGAAAAAAAAAA 1289
          |||||||||||||||||||||||||    | ||
Db    924 GCAGAGAATAAAGTGTTCTATGAAATTCAGAA 955


RESULT 11
AX179609
LOCUS       AX179609               2149 bp    DNA     linear   PAT 06-AUG-2001
DEFINITION  Sequence 32 from Patent WO0146422.
ACCESSION   AX179609
VERSION     AX179609.1  GI:15132038
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2149)
  AUTHORS   Presnell,S.R. and Kindsvogel,W.
  TITLE     Cytokine zcyto18
  JOURNAL   Patent: WO 0146422-A 32 28-JUN-2001;
            ZymoGenetics, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .2149
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
     CDS             1. .696
                     /note="unnamed protein product"
                     /codon_start=1
                     /protein_id="CAC49975.1"
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                     /db_xref="GI:15132039"
                     /translation="MMPKHCFLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNI
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                     VRAASAGSYSEWSMTPRFTPWWETKIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKN
                     VSIEDYYELLYRVFIINNSLEKEQKVYEGAHRAVEIEALTPHSSYCVVAEIYQPMLDR
                     RSQRSEERCVEIP"
BASE COUNT      685 a    381 c    421 g    662 t
ORIGIN

  Query Match           63.1%;  Score 831.6;  DB 6;  Length 2149;
  Best Local Similarity 90.4%;  Pred. No. 6.1e-169;
  Matches  951;  Conservative    0;  Mismatches    4;  Indels   97;  Gaps    2;

Qy     238 ATGATGCCTAAACATTGCTTTCTAGGCTTCCTCATCAGTTTCTTCCTTACTGGTGTAGCA 297
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 ATGATGCCTAAACATTGCTTTCTAGGCTTCCTCATCAGTTTCTTCCTTACTGGTGTAGCA 60

Qy     298 GGAACTCAGTCAACGCATGAGTCTCTGAAGCCTCAGAGGGTACAATTTCAGTCCCGAAAT 357
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 GGAACTCAGTCAACGCATGAGTCTCTGAAGCCTCAGAGGGTACAATTTCAGTCCCGAAAT 120

Qy     358 TTTCACAACATTTTGCAATGGCAGCCTGGGAGGGCACTTACTGGCAACAGCAGTGTCTAT 417
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 TTTCACAACATTTTGCAATGGCAGCCTGGGAGGGCACTTACTGGCAACAGCAGTGTCTAT 180

Qy     418 TTTGTGCAGTACAAAATCATGTTCTCATGCAGCATGAAAAGCTCTCACCAGAAGCCAAGT 477
           ||||||||||||||||
Db     181 TTTGTGCAGTACAAAAT---------------------------------------------- 197

Qy     478 GGATGCTGGCAGCACATTTCTTGTAACTTCCCAGGCTGCAGAACATTGGCTAAATATGGA 537
                                                             |||||||
Db     198 ----------------------------------------------------ATATGGA 204

Qy     538 CAGAGACAATGGAAAAATAAAGAAGACTGTTGGGGTACTCAAGAACTCTCTTGTGACCTT 597
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     205 CAGAGACAATGGAAAAATAAAGAAGACTGTTGGGGTACTCAAGAACTCTCTTGTGACCTT 264

Qy     598 ACCAGTGAAACCTCAGACATACAGGAACCTTATTACGGGAGGGTGAGGGCGGCCTCGGCT 657
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Db     265 ACCAGTGAAACCTCAGACATACAGGAACCTTATTACGGGAGGGTGAGGGCGGCCTCGGCT 324

Qy     658 GGGAGCTACTCAGAATGGAGCATGACGCCGCGGTTCACTCCCTGGTGGGAAACAAAAATA 717
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     325 GGGAGCTACTCAGAATGGAGCATGACGCCGCGGTTCACTCCCTGGTGGGAAACAAAAATA 384

Qy     718 GATCCTCCAGTCATGAATATAACCCAAGTCAATGGCTCTTTGTTGGTAATTCTCCATGCT 777
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     385 GATCCTCCAGTCATGAATATAACCCAAGTCAATGGCTCTTTGTTGGTAATTCTCCATGCT 444

Qy     778 CCAAATTTACCATATAGATACCAAAAGGAAAAAAATGTATCTATAGAAGATTACTATGAA 837
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     445 CCAAATTTACCATATAGATACCAAAAGGAAAAAAATGTATCTATAGAAGATTACTATGAA 504

Qy     838 CTACTATACCGAGTTTTTATAATTAACAATTCACTAGAAAAGGAGCAAAAGGTTTATGAA 897
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     505 CTACTATACCGAGTTTTTATAATTAACAATTCACTAGAAAAGGAGCAAAAGGTTTATGAA 564

Qy     898 GGGGCTCACAGAGCGGTTGAAATTGAAGCTCTAACACCACACTCCAGCTACTGTGTAGTG 957
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     565 GGGGCTCACAGAGCGGTTGAAATTGAAGCTCTAACACCACACTCCAGCTACTGTGTAGTG 624

Qy     958 GCTGAAATATATCAGCCCATGTTAGACAGAAGAAGTCAGAGAAGTGAAGAGAGATGTGTG 1017
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Db     625 GCTGAAATATATCAGCCCATGTTAGACAGAAGAAGTCAGAGAAGTGAAGAGAGATGTGTG 684

Qy    1018 GAAATTCCATGACTTGTGGAATTTGGCATTCAGCAATGTGGAAATTCTAAAGCTCCCTGA 1077
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     685 GAAATTCCATGACTTGTGGAATTTGGCATTCAGCAATGTGGAAATTCTAAAGCTCCCTGA 744

Qy    1078 GAACAGGATGACTCGTGTTTGAAGGATCTTATTTAAAATTGTTTTTGTATTTTCTTAAAG 1137
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     745 GAACAGGATGACTCGTGTTTGAAGGATCTTATTTAAAATTGTTTTTGTATTTTCTTAAAG 804

Qy    1138 CAATATTCACTGTTACACCTTGGGGACTTCTTTGTTTATCCATTCTTTTATCCTTTATAT 1197
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     805 CAATATTCACTGTTACACCTTGGGGACTTCTTTGTTTATCCATTCTTTTATCCTTTATAT 864

Qy    1198 TTCATTTGTAAACTATATTTGAACGACATTCCCCCCGAAAAATTGAAATGTAAAGATGAG 1257
           ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     865 TTCATTT-TAAACTATATTTGAACGACATTCCCCCCGAAAAATTGAAATGTAAAGATGAG 923

Qy    1258 GCAGAGAATAAAGTGTTCTATGAAAAAAAAAA 1289
           |||||||||||||||||||||||||    | ||
Db     924 GCAGAGAATAAAGTGTTCTATGAAATTCAGAA 955


RESULT 12
AX399656
LOCUS       AX399656                 810 bp    DNA     linear   PAT 06-JUN-2002
DEFINITION  Sequence 5 from Patent EP1191035.
ACCESSION   AX399656
VERSION     AX399656.1  GI:21335432
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Weiss,B., Sabat,R., Assadullah,K. and Toshi,L.
  TITLE     Three members of the cytokin-receptor class II family
  JOURNAL   Patent: EP 1191035-A 5 27-MAR-2002;
            SCHERING AKTIENGESELLSCHAFT (DE)
FEATURES             Location/Qualifiers
     source          1. .810
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT      253 a    172 c    184 g    201 t
ORIGIN

  Query Match           61.1%;  Score 805.2;  DB 6;  Length 810;
  Best Local Similarity 99.6%;  Pred. No. 3e-163;
  Matches  807;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy     227 CACTTGCAACCATGATGCCTAAACATTGCTTTCTAGGCTTCCTCATCAGTTTCTTCCTTA 286
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 CACTTGCAACCATGATGCCTAAACATTGCTTTCTAGGCTTCCTCATCAGTTTCTTCCTTA 60

Qy     287 CTGGTGTAGCAGGAACTCAGTCAACGCATGAGTCTCTGAAGCCTCAGAGGGTACAATTTC 346
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 CTGGTGTAGCAGGAACTCAGTCAACGCATGAGTCTCTGAAGCCTCAGAGGGTACAATTTC 120

Qy     347 AGTCCCGAAATTTTCACAACATTTTGCAATGGCAGCCTGGGAGGGCACTTACTGGCAACA 406
           |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db     121 AGTCCCGAAATTTTCACAACATTTTGCAATGGCAGCCGGGGAGGGCACTTACTGGCAACA 180

Qy     407 GCAGTGTCTATTTTGTGCAGTACAAAATCATGTTCTCATGCAGCATGAAAAGCTCTCACC 466
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 GCAGTGTCTATTTTGTGCAGTACAAAATCATGTTCTCATGCAGCATGAAAAGCTCTCACC 240

Qy     467 AGAAGCCAAGTGGATGCTGGCAGCACATTTCTTGTAACTTCCCAGGCTGCAGAACATTGG 526
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Db     241 AGAAGCCAAGTGGATGCTGGCAGCACATTTCTTGTAACTTCCCAGGCTGCAGAACATTGG 300

Qy     527 CTAAATATGGACAGAGACAATGGAAAAATAAAGAAGACTGTTGGGGTACTCAAGAACTCT 586
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 CTAAATATGGACAGAGACAATGGAAAAATAAAGAAGACTGTTGGGGTACTCAAGAACTCT 360

Qy     587 CTTGTGACCTTACCAGTGAAACCTCAGACATACAGGAACCTTATTACGGGAGGGTGAGGG 646
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 CTTGTGACCTTACCAGTGAAACCTCAGACATACAGGAACCTTATTACGGGAGGGTGAGGG 420

Qy     647 CGGCCTCGGCTGGGAGCTACTCAGAATGGAGCATGACGCCGCGGTTCACTCCCTGGTGGG 706
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 CGGCCTCGGCTGGGAGCTACTCAGAATGGAGCATGACGCCGCGGTTCACTCCCTGGTGGG 480

Qy     707 AAACAAAAATAGATCCTCCAGTCATGAATATAACCCAAGTCAATGGCTCTTTGTTGGTAA 766
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Db     481 AAACAAAAATAGATCCTCCAGTCATGAATATAACCCAAGTCAATGGCTCTTTGTTGGTAA 540

Qy     767 TTCTCCATGCTCCAAATTTACCATATAGATACCAAAAGGAAAAAAATGTATCTATAGAAG 826
           |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 TTCTCCATGCCCCAAATTTACCATATAGATACCAAAAGGAAAAAAATGTATCTATAGAAG 600

Qy     827 ATTACTATGAACTACTATACCGAGTTTTTATAATTAACAATTCACTAGAAAAGGAGCAAA 886
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 ATTACTATGAACTACTATACCGAGTTTTTATAATTAACAATTCACTAGAAAAGGAGCAAA 660

Qy     887 AGGTTTATGAAGGGGCTCACAGAGCGGTTGAAATTGAAGCTCTAACACCACACTCCAGCT 946
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 AGGTTTATGAAGGGGCTCACAGAGCGGTTGAAATTGAAGCTCTAACACCACACTCCAGCT 720

Qy     947 ACTGTGTAGTGGCTGAAATATATCAGCCCATGTTAGACAGAAGAAGTCAGAGAAGTGAAG 1006
           |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db     721 ACTGTGTAGTGGCTGAAATATATCAGCCCATGTTAGACAGAAGAAGTCGGAGAAGTGAAG 780

Qy    1007 AGAGATGTGTGGAAATTCCATGACTTGTGG 1036
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Db     781 AGAGATGTGTGGAAATTCCATGACTTGTGG 810
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RESULT 13
AY040568

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LOCUS       AY040568                2593 bp    mRNA    linear   PRI 19-AUG-2001
DEFINITION  Homo sapiens interleukin 22-binding protein CRF2-10S (IL22BP) mRNA,
            complete cds, alternatively spliced.
ACCESSION   AY040568
VERSION     AY040568.1  GI:15212829
KEYWORDS    .
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2593)
  AUTHORS   Kotenko,S.V., Izotova,L.S., Mirochnitchenko,O.V., Esterova,E.,
            Dickensheets,H., Donnelly,R.P. and Pestka,S.
  TITLE     Identification, cloning, and characterization of a novel soluble
            receptor that binds IL-22 and neutralizes its activity
  JOURNAL   J. Immunol. 166 (12), 7096-7103 (2001)
  MEDLINE   21286453
   PUBMED   11390454
REFERENCE   2  (bases 1 to 2593)
  AUTHORS   Kotenko,S.V. and Pestka,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-JUN-2001) Molecular Genetics and Microbiology,
            UMDNJ-Robert Wood Johnson Medical School, 675 Hoes Lane,
            Piscataway, NJ 08854-5635, USA
FEATURES             Location/Qualifiers
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Query Match 55.4%; Score 730.6; DB 9; Length 2593;

Best Local Similarity 79.1%; Pred. No. 3.5e-147;
Matches 1019; Conservative 0; Mismatches 4; Indels 266; Gaps 2;

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Qy      61 GGATTAACAAAGACAAAATATGGGAAAAACATAACATGGCGTCCCATAATTATTAGATCT 120
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Qy     121 TATTATTGACACTAAAATGGCATTAAAATTACCAAAAGGAAGACAGCATCTGTTTCCTCT 180
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Qy     601 AGTGAAACCTCAGACATACAGGAACCTTATTACGGGAGGGTGAGGGCGGCCTCGGCTGGG 660
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Qy     661 AGCTACTCAGAATGGAGCATGACGCCGCGGTTCACTCCCTGGTGGGAAACAAAAATAGAT 720
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Qy    1141 TATTCACTGTTACACCTTGGGGACTTCTTTGTTTATCCATTCTTTTATCCTTTATATTTC 1200
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RESULT 14
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LOCUS HSA297262 775 bp mRNA linear PRI 19-DEC-2001
DEFINITION Homo sapiens mRNA for interleukin-22 binding protein (IL-22BP gene).
ACCESSION AJ297262
VERSION AJ297262.1 GI:17974196
KEYWORDS IL-22BP gene; interleukin-22 binding protein.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Dumoutier,L., Lejeune,D. and Renauld,J.C.
TITLE Cloning and characterization of Interelukin-22 Binding Protein (IL-22BP), a natural antagonist of IL-TIF/IL-22
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 775)
AUTHORS Renauld,J.C.
TITLE Direct Submission
JOURNAL Submitted (19-DEC-2000) Renauld J.C., UCL 74.59, Ludwig Institute for Cancer Research, Avenue Hippocrate, 74, B-1200 Brussels, BELGIUM
FEATURES Location/Qualifiers
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BASE COUNT 248 a 157 c 175 g 195 t
ORIGIN

Query Match 50.8%; Score 669; DB 9; Length 775;
Best Local Similarity 89.0%; Pred. No. 6.7e-134;
Matches 775; Conservative 0; Mismatches 0; Indels 96; Gaps 1;

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RESULT 15
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LOCUS AX193705 696 bp DNA linear PAT 15-AUG-2001
DEFINITION Sequence 27 from Patent WO0136467.
ACCESSION AX193705
VERSION AX193705.1 GI:15211554
KEYWORDS .
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 696)
AUTHORS Gorman,D.M.
TITLE Mammalian receptor proteins; related reagents and methods
JOURNAL Patent: WO 0136467-A 27 25-MAY-2001;
SCHERING CORPORATION (US)
FEATURES Location/Qualifiers
source 1. .696

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Db    205 CAGAGACAATGGAAAAATAAAGAAGACTGTTGGGGTACTCAAGAACTCTCTTGTGACCTT 264

Qy    598 ACCAGTGAAACCTCAGACATACAGGAACCTTATTACGGGAGGGTGAGGGCGGCCTCGGCT 657
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Job time : 2790 secs
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GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: December 22, 2002, 06:48:36 ; Search time 252 Seconds
(without alignments)
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Sequence: 1 cagtttcttcatctgtaaca.....aaaaaaaaaaaaaaaaaaaa 1318

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	4	1078.4	81.8	1255	24	AAL46000	Human cytokine rec
	5	910	69.0	2271	24	ABK50076	DNA encoding human
	6	831.6	63.1	2149	22	AAD09745	Human ZCYTO18 solu
	7	831.6	63.1	2149	22	AAF83735	Human cytokine rec
	8	805.2	61.1	810	24	AAL46001	Human cytokine rec
	9	792	60.1	792	24	AAD27816	Human cytokine rec
	10	590	44.8	696	24	AAD27815	Human cytokine rec
	11	588.4	44.6	696	22	AAD06414	Human DNAX cytokin
	12	533	40.4	645	24	AAD27814	Human cytokine rec
	13	449.2	34.1	750	22	AAD06410	Human DNAX cytokin
	14	449.2	34.1	750	24	AAL45999	Human cytokine rec
	15	398.2	30.2	693	22	AAD06415	Human DNAX cytokin
	16	398.2	30.2	693	22	AAF83736	Human cytokine rec
	17	319.6	24.2	747	22	AAD06411	Human DNAX cytokin
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	19	197.8	15.0	298	24	AAL46018	Rat cytokine recep
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	36	166.2	12.6	390	22	AAD06417	Human DNAX cytokin
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	40	75.4	5.7	1806	22	AAH22834	Mouse IL-20 recept
	41	75.4	5.7	1806	24	ABK96195	DNA encoding mouse
	42	71	5.4	550	23	ABV57072	Human prostate exp
c	43	70	5.3	348	22	AAL10133	Human breast cance
	44	67.2	5.1	309	23	ABV44994	Human prostate exp
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ALIGNMENTS

RESULT 1
AAS15368
ID AAS15368 standard; cDNA; 1318 BP.
XX
AC AAS15368;
XX
DT 16-JAN-2002 (first entry)
XX
DE cDNA encoding human PRO19598 polypeptide.
XX
KW Human; PRO19598; clone DNA145887; immune-related disorder;
KW inflammatory disorder; infectious disorder; immunodeficiency disorder;
KW autoimmune disorder; renal disease; demyelinating disease; skin disease;
KW neoplasia; transplantation associated disease; gene therapy;
KW immunosuppressive; anti-inflammatory; antiasthmatic; antidiabetic; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 241..1029
FT /*tag= a
FT /product= "PRO19598 polypeptide"
FT sig_peptide 241..300
FT /*tag= b
FT mat_peptide 301..1026
FT /*tag= c
XX
PN WO200166740-A2.
XX
PD 13-SEP-2001.
XX
PF 01-MAR-2001; 2001WO-US06666.

XX
PR 03-MAR-2000; 2000US-187202P.
PR 21-MAR-2000; 2000US-191015P.
PR 30-MAY-2000; 2000WO-US14941.
PR 05-JUN-2000; 2000US-209832P.
PR 24-AUG-2000; 2000WO-US23328.
PR 01-DEC-2000; 2000WO-US32678.
XX
PA (GETH) GENENTECH INC.
XX
PI Eaton DL, Fong S, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL;
PI Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2001-625876/72.
DR P-PSDB; AAU09186.
XX
PT Nucleic acids encoding PRO polypeptides, useful for detecting and
PT treating immune related diseases and disorders in mammals including
PT autoimmune diseases, inflammatory diseases and asthma -
XX
Claim 2; Fig 17; 122pp; English.
XX
CC The present invention relates to the isolation of 9 novel human PRO
CC polypeptides (AAU09178-AAU09186) and the cDNA sequences encoding them.
CC The novel PRO polypeptides include PRO1356, PRO1268, PRO1884, PRO3444,
CC PRO3151, PRO4322, PRO9964, PRO10008 and PRO19598. The cDNA sequences
CC encoding these PRO polypeptides have been designated as clones
CC DNA64886-1601, DNA64903-1553, DNA84318-2520, DNA87997, DNA89273,
CC DNA92223-2567, DNA96973, DNA101921 and DNA145887 respectively.
CC Compositions (e.g. vaccines) containing PRO polypeptides and methods of
CC using these compositions are useful in the treatment and diagnosis of
CC immune-related disorders. Such disorders include immune-mediated
CC inflammatory disorders (e.g. osteoarthritis), non-immune-mediated
CC inflammatory disorders (e.g. diabetes mellitus), infectious disorders
CC (e.g. granulomatous hepatitis), immunodeficiency disorders (e.g. AIDS),
CC autoimmune disorders (e.g. rheumatoid arthritis), immune-related renal
CC diseases (e.g. cirrhosis), demyelinating diseases of the peripheral or
CC central nervous system (e.g. Guillain-Barre syndrome), immune-mediated
CC skin diseases (e.g. contact dermatitis), neoplasias and transplantation
CC associated diseases. The polynucleotide sequences of the invention may
CC be used in gene therapy. AAS15360-AAS15368 represent cDNA sequences
CC encoding for the novel human PRO polypeptides of the invention.
XX
SQ Sequence 1318 BP; 451 A; 251 C; 259 G; 357 T; 0 other;

Query Match 100.0%; Score 1318; DB 22; Length 1318;
Best Local Similarity 100.0%; Pred. No. 5.3e-263;
Matches 1318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1 CAGTTTCTTCATCTGTAACATCAAATGAATAATAATACCAATCTCCTAGACTTCATAAGA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 CAGTTTCTTCATCTGTAACATCAAATGAATAATAATACCAATCTCCTAGACTTCATAAGA 60

Qy      61 GGATTAACAAAGACAAAATATGGGAAAAACATAACATGGCGTCCCATAATTATTAGATCT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 GGATTAACAAAGACAAAATATGGGAAAAACATAACATGGCGTCCCATAATTATTAGATCT 120

Qy     121 TATTATTGACACTAAAATGGCATTAAAATTACCAAAAGGAAGACAGCATCTGTTTCCTCT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 TATTATTGACACTAAAATGGCATTAAAATTACCAAAAGGAAGACAGCATCTGTTTCCTCT 180

Qy     181 TTGGTCCTGAGCTGGTTAAAAGGAACACTGGTTGCCTGAACAGTCACACTTGCAACCATG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 TTGGTCCTGAGCTGGTTAAAAGGAACACTGGTTGCCTGAACAGTCACACTTGCAACCATG 240

Qy     241 ATGCCTAAACATTGCTTTCTAGGCTTCCTCATCAGTTTCTTCCTTACTGGTGTAGCAGGA 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 ATGCCTAAACATTGCTTTCTAGGCTTCCTCATCAGTTTCTTCCTTACTGGTGTAGCAGGA 300

Qy     301 ACTCAGTCAACGCATGAGTCTCTGAAGCCTCAGAGGGTACAATTTCAGTCCCGAAATTTT 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 ACTCAGTCAACGCATGAGTCTCTGAAGCCTCAGAGGGTACAATTTCAGTCCCGAAATTTT 360

Qy     361 CACAACATTTTGCAATGGCAGCCTGGGAGGGCACTTACTGGCAACAGCAGTGTCTATTTT 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 CACAACATTTTGCAATGGCAGCCTGGGAGGGCACTTACTGGCAACAGCAGTGTCTATTTT 420

Qy     421 GTGCAGTACAAAATCATGTTCTCATGCAGCATGAAAAGCTCTCACCAGAAGCCAAGTGGA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 GTGCAGTACAAAATCATGTTCTCATGCAGCATGAAAAGCTCTCACCAGAAGCCAAGTGGA 480

Qy     481 TGCTGGCAGCACATTTCTTGTAACTTCCCAGGCTGCAGAACATTGGCTAAATATGGACAG 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 TGCTGGCAGCACATTTCTTGTAACTTCCCAGGCTGCAGAACATTGGCTAAATATGGACAG 540

Qy     541 AGACAATGGAAAAATAAAGAAGACTGTTGGGGTACTCAAGAACTCTCTTGTGACCTTACC 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 AGACAATGGAAAAATAAAGAAGACTGTTGGGGTACTCAAGAACTCTCTTGTGACCTTACC 600

Qy     601 AGTGAAACCTCAGACATACAGGAACCTTATTACGGGAGGGTGAGGGCGGCCTCGGCTGGG 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 AGTGAAACCTCAGACATACAGGAACCTTATTACGGGAGGGTGAGGGCGGCCTCGGCTGGG 660

Qy     661 AGCTACTCAGAATGGAGCATGACGCCGCGGTTCACTCCCTGGTGGGAAACAAAAATAGAT 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 AGCTACTCAGAATGGAGCATGACGCCGCGGTTCACTCCCTGGTGGGAAACAAAAATAGAT 720

Qy     721 CCTCCAGTCATGAATATAACCCAAGTCAATGGCTCTTTGTTGGTAATTCTCCATGCTCCA 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 CCTCCAGTCATGAATATAACCCAAGTCAATGGCTCTTTGTTGGTAATTCTCCATGCTCCA 780

Qy     781 AATTTACCATATAGATACCAAAAGGAAAAAAATGTATCTATAGAAGATTACTATGAACTA 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 AATTTACCATATAGATACCAAAAGGAAAAAAATGTATCTATAGAAGATTACTATGAACTA 840

Qy     841 CTATACCGAGTTTTTATAATTAACAATTCACTAGAAAAGGAGCAAAAGGTTTATGAAGGG 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 CTATACCGAGTTTTTATAATTAACAATTCACTAGAAAAGGAGCAAAAGGTTTATGAAGGG 900

Qy     901 GCTCACAGAGCGGTTGAAATTGAAGCTCTAACACCACACTCCAGCTACTGTGTAGTGGCT 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 GCTCACAGAGCGGTTGAAATTGAAGCTCTAACACCACACTCCAGCTACTGTGTAGTGGCT 960

Qy     961 GAAATATATCAGCCCATGTTAGACAGAAGAAGTCAGAGAAGTGAAGAGAGATGTGTGGAA 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 GAAATATATCAGCCCATGTTAGACAGAAGAAGTCAGAGAAGTGAAGAGAGATGTGTGGAA 1020

Qy    1021 ATTCCATGACTTGTGGAATTTGGCATTCAGCAATGTGGAAATTCTAAAGCTCCCTGAGAA 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 ATTCCATGACTTGTGGAATTTGGCATTCAGCAATGTGGAAATTCTAAAGCTCCCTGAGAA 1080

Qy    1081 CAGGATGACTCGTGTTTGAAGGATCTTATTTAAAATTGTTTTTGTATTTTCTTAAAGCAA 1140
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Db    1081 CAGGATGACTCGTGTTTGAAGGATCTTATTTAAAATTGTTTTTGTATTTTCTTAAAGCAA 1140

Qy    1141 TATTCACTGTTACACCTTGGGGACTTCTTTGTTTATCCATTCTTTTATCCTTTATATTTC 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141 TATTCACTGTTACACCTTGGGGACTTCTTTGTTTATCCATTCTTTTATCCTTTATATTTC 1200

Qy    1201 ATTTGTAAACTATATTTGAACGACATTCCCCCCGAAAAATTGAAATGTAAAGATGAGGCA 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201 ATTTGTAAACTATATTTGAACGACATTCCCCCCGAAAAATTGAAATGTAAAGATGAGGCA 1260

Qy    1261 GAGAATAAAGTGTTCTATGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1318
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1261 GAGAATAAAGTGTTCTATGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1318
```

RESULT 2
ABK50080
ID ABK50080 standard; DNA; 2367 BP.
XX
AC ABK50080;
XX
DT 15-JUL-2002 (first entry)
XX

DE DNA encoding human IL-TIF/IL-22 binding protein #2.
XX
KW Human; soluble protein; interleukin-TIF/IL-22; IL-TIF/IL-22; IL-22BP;
KW IL-TIF/IL-22 antagonist; gene; ds.
XX
OS Homo sapiens.
XX

FH Key Location/Qualifiers
FT CDS 110..900
FT /*tag= a
FT /product= "Human IL-TIF/IL-22 binding protein #2"
FT /note= "This sequence can optionally start at
FT position 113"
XX
PN WO200224912-A2.
XX
PD 28-MAR-2002.
XX
PF 21-SEP-2001; 2001WO-US29576.

[redacted]
22-SEP-2000; 2000US-234583P.
03-NOV-2000; 2000US-245495P.
PR 31-JUL-2001; 2001US-0919162.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Renauld J, Dumoutier L;
XX
DR WPI; 2002-383190/41.
DR P-PSDB; AAU80324.
XX
PT Polynucleotide and polypeptide of soluble protein which binds to
PT interleukin-TIF/IL-22 useful for inhibiting effect of IL-TIF/IL-22 on a
PT cell -
XX
PS Claim 1; Page 40-41; 42pp; English.
XX
CC The present invention relates to a new polynucleotide that encodes a
CC soluble protein which binds to interleukin (IL)-TIF/IL-22 (also referred
CC to as IL-22BP), where the complementary sequence of the invention
CC hybridises under stringent conditions to a nucleotide sequence of 2271
CC or 2366 base pairs, as given in the specification. The molecules of the
CC invention are useful for inhibiting (antagonising) effect of IL-TIF/IL-22
CC on a cell, for determining whether IL-TIF/IL-22 is present in a sample,
CC for inhibiting binding of IL-TIF/IL-22 to a binding partner, preferably
CC in vitro, and for obtaining an antibody molecule specific for the soluble
CC binding protein of the invention, from a population or panel of antibody
CC molecules of diverse binding specificity. The soluble protein is further
CC useful in manufacture of a medicament for treating an IL-22 mediated
CC disease and for assaying an agent, preferably an antibody or a peptide
CC fragment of IL-TIF/IL-22 or the soluble protein, that modulates binding
CC of the soluble protein to IL-TIF/IL-22, where the agent identified is
CC used in the manufacture of medicament for treating IL-TIF/IL-22 mediated
CC disorder. The antibody is useful for determining presence of the soluble
CC protein, where the antibody is detectably labelled. The present nucleic
CC acid sequence encodes the human IL-TIF/IL-22 binding protein #2 of the
CC invention.
XX
SQ Sequence 2367 BP; 735 A; 425 C; 465 G; 742 T; 0 other;

Query Match 83.0%; Score 1094.4; DB 24; Length 2367;
Best Local Similarity 98.6%; Pred. No. 9.3e-217;
Matches 1104; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

```
Qy    170 CTGTTTCCTCTTTGGTCCTGAGCTGGTTAAAAGGAACACTGGTTGCCTGAACAGTCACAC 229
          | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     42 CAGTTTCCTCTTTGGTCCTGAGCTGGTTAAAAGGAACACTGGTTGCCTGAACAGTCACAC 101

Qy    230 TTGCAACCATGATGCCTAAACATTGCTTTCTAGGCTTCCTCATCAGTTTCTTCCTTACTG 289
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    102 TTGCAACCATGATGCCTAAACATTGCTTTCTAGGCTTCCTCATCAGTTTCTTCCTTACTG 161

Qy    290 GTGTAGCAGGAACTCAGTCAACGCATGAGTCTCTGAAGCCTCAGAGGGTACAATTTCAGT 349
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    162 GTGTAGCAGGAACTCAGTCAACGCATGAGTCTCTGAAGCCTCAGAGGGTACAATTTCAGT 221

Qy    350 CCCGAAATTTTCACAACATTTTGCAATGGCAGCCTGGGAGGGCACTTACTGGCAACAGCA 409
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    222 CCCGAAATTTTCACAACATTTTGCAATGGCAGCCTGGGAGGGCACTTACTGGCAACAGCA 281

Qy    410 GTGTCTATTTTGTGCAGTACAAAATCATGTTCTCATGCAGCATGAAAAGCTCTCACCAGA 469
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    282 GTGTCTATTTTGTGCAGTACAAAATCATGTTCTCATGCAGCATGAAAAGCTCTCACCAGA 341

Qy    470 AGCCAAGTGGATGCTGGCAGCACATTTCTTGTAACTTCCCAGGCTGCAGAACATTGGCTA 529
            | |   |     ||||||||||||||||||||||||||||||||||||||||||||||
Db    342 GCCAAGTGGATGCTTGGCAGCACATTTCTTGTAACTTCCCAGGCTGCAGAACATTGGCTA 401

Qy    530 AATATGGACAGAGACAATGGAAAAATAAAGAAGACTGTTGGGGTACTCAAGAACTCTCTT 589
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Db    402 AATATGGACAGAGACAATGGAAAAATAAAGAAGACTGTTGGGGTACTCAAGAACTCTCTT 461

Qy    590 GTGACCTTACCAGTGAAACCTCAGACATACAGGAACCTTATTACGGGAGGGTGAGGGCGG 649
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    462 GTGACCTTACCAGTGAAACCTCAGACATACAGGAACCTTATTACGGGAGGGTGAGGGCGG 521

Qy    650 CCTCGGCTGGGAGCTACTCAGAATGGAGCATGACGCCGCGGTTCACTCCCTGGTGGGAAA 709
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Db    522 CCTCGGCTGGGAGCTACTCAGAATGGAGCATGACGCCGCGGTTCACTCCCTGGTGGGAAA 581

Qy    710 CAAAAATAGATCCTCCAGTCATGAATATAACCCAAGTCAATGGCTCTTTGTTGGTAATTC 769
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Db    582 CAAAAATAGATCCTCCAGTCATGAATATAACCCAAGTCAATGGCTCTTTGTTGGTAATTC 641

Qy    770 TCCATGCTCCAAATTTACCATATAGATACCAAAAGGAAAAAAATGTATCTATAGAAGATT 829
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    642 TCCATGCTCCAAATTTACCATATAGATACCAAAAGGAAAAAAATGTATCTATAGAAGATT 701

Qy    830 ACTATGAACTACTATACCGAGTTTTTATAATTAACAATTCACTAGAAAAGGAGCAAAAGG 889
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    702 ACTATGAACTACTATACCGAGTTTTTATAATTAACAATTCACTAGAAAAGGAGCAAAAGG 761

Qy    890 TTTATGAAGGGGCTCACAGAGCGGTTGAAATTGAAGCTCTAACACCACACTCCAGCTACT 949
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    762 TTTATGAAGGGGCTCACAGAGCGGTTGAAATTGAAGCTCTAACACCACACTCCAGCTACT 821

Qy    950 GTGTAGTGGCTGAAATATATCAGCCCATGTTAGACAGAAGAAGTCAGAGAAGTGAAGAGA 1009
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    822 GTGTAGTGGCTGAAATATATCAGCCCATGTTAGACAGAAGAAGTCAGAGAAGTGAAGAGA 881

Qy   1010 GATGTGTGGAAATTCCATGACTTGTGGAATTTGGCATTCAGCAATGTGGAAATTCTAAAG 1069
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    882 GATGTGTGGAAATTCCATGACTTGTGGAATTTGGCATTCAGCAATGTGGAAATTCTAAAG 941

Qy   1070 CTCCCTGAGAACAGGATGACTCGTGTTTGAAGGATCTTATTTAAAATTGTTTTTGTATTT 1129
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Db    942 CTCCCTGAGAACAGGATGACTCGTGTTTGAAGGATCTTATTTAAAATTGTTTTTGTATTT 1001

Qy   1130 TCTTAAAGCAATATTCACTGTTACACCTTGGGGACTTCTTTGTTTATCCATTCTTTTATC 1189
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1002 TCTTAAAGCAATATTCACTGTTACACCTTGGGGACTTCTTTGTTTATCCATTCTTTTATC 1061

Qy   1190 CTTTATATTTCATTTGTAAACTATATTTGAACGACATTCCCCCCGAAAAATTGAAATGTA 1249
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1062 CTTTATATTTCATTTGTAAACTATATTTGAACGACATTCCCCCCGAAAAATTGAAATGTA 1121

Qy   1250 AAGATGAGGCAGAGAATAAAGTGTTCTATGAAAAAAAAAA 1289
          ||||||||||||||||||||||||||||||||||   | ||
Db   1122 AAGATGAGGCAGAGAATAAAGTGTTCTATGAAATTCAGAA 1161
```

RESULT 3
ABK70017
ID ABK70017 standard; DNA; 1389 BP.
XX
AC ABK70017;

XX
DT 15-JUL-2002 (first entry)
XX
DE cDNA encoding human Pro peptide #57.
XX
KW Human; ss; gene; PRO; secreted protein; transmembrane protein;
KW genetic disorder; tumour; cancer.
XX
OS Homo sapiens.
XX
PN WO200224888-A2.
XX
PD 28-MAR-2002.
XX
PF 29-AUG-2001; 2001WO-US27099.
XX
PR 01-SEP-2000; 2000US-229896P.
PR 05-SEP-2000; 2000US-230621P.
PR 22-SEP-2000; 2000US-235147P.
PR 10-NOV-2000; 2000WO-US30873.
PR 12-JAN-2001; 2001US-261878P.
PR 16-JAN-2001; 2001US-261910P.
PR 16-JAN-2001; 2001US-261939P.
PR 16-JAN-2001; 2001US-262150P.
PR 25-JAN-2001; 2001US-264395P.
PR 02-FEB-2001; 2001US-266421P.
PR 09-FEB-2001; 2001US-267623P.
PR 28-FEB-2001; 2001WO-US06520.
PR 09-MAR-2001; 2001US-274399P.
PR 03-APR-2001; 2001US-280982P.
PR 04-APR-2001; 2001US-282129P.
PR 04-APR-2001; 2001US-282199P.
PR 09-MAY-2001; 2001US-290589P.
PR 25-MAY-2001; 2001WO-US17092.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;
PI Gurney AL, Smith V, Stephan J, Watanabe CK, Wood WI, Zhang Z;
PI Fong S;
XX
DR WPI; 2002-362426/39.
DR P-PSDB; ABG34086.
XX
PT New PRO polypeptides and polynucleotides encoding the polypeptides,
PT useful in gene therapy, chromosome identification, tissue typing, or
PT for genetic analysis of individuals with genetic disorders -
XX
PS Claim 2; Figure 113; 218pp; English.
XX
CC This invention relates to the cDNA and protein sequences of novel
CC secreted and transmembrane polypeptides PRO polypeptides. The
CC invention also comprises a method for producing the proteins of the
CC invention by recombinant means and antibodies specific for the protein
CC of the invention. The antibody may be used for detecting the PRO
CC proteins of the invention and may be used to modify their activity.
CC polynucleotides may be used as hybridisation probes for a cDNA library
CC to isolate the full-length PRO cDNA or to isolate other cDNAs, to
CC construct hybridisation probes for mapping the gene which encodes that
CC PRO and for genetic analysis of individuals with genetic disorders, in
CC assays to identify other proteins or molecules involved in binding
CC reaction, to generate transgenic animals or knock-out animals which in
CC turn are useful in the development and screening of therapeutically
CC useful reagents, for chromosome identification, and tissue typing. The
CC PRO polypeptides are useful in gene therapy, and as molecular weight
CC markers for protein electrophoresis purposes. The sequences may
CC also be used to detect overexpression on PRO polypeptides in cancerous
CC tumours and for screening for differentially expressed genes using
CC microarray technology. The present sequence represents a cDNA encoding
CC a human PRO protein of the invention.
XX
SQ Sequence 1389 BP; 460 A; 269 C; 260 G; 400 T; 0 other;

Query Match 81.9%; Score 1079; DB 24; Length 1389;
Best Local Similarity 92.2%; Pred. No. 1.3e-213;
Matches 1188; Conservative 0; Mismatches 5; Indels 96; Gaps 1;

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Qy       1 CAGTTTCTTCATCTGTAACATCAAATGAATAATAATACCAATCTCCTAGACTTCATAAGA 60
Db      63 CAGTTTCTTCATCTGTAACATCAAATGAATAATAATACCAATCTCCTAGACTTCATAAGA 122

Qy      61 GGATTAACAAAGACAAAATATGGGAAAAACATAACATGGCGTCCCATAATTATTAGATCT 120
Db     123 GGATTAACAAAGACAAAATATGGGAAAAACATAACATGGCGTCCCATAATTATTAGATCT 182

Qy     121 TATTATTGACACTAAAATGGCATTAAAATTACCAAAAGGAAGACAGCATCTGTTTCCTCT 180
Db     183 TATTATTGACACTAAAATGGCATTAAAATTACCAAAAGGAAGACAGCATCTGTTTCCTCT 242

Qy     181 TTGGTCCTGAGCTGGTTAAAAGGAACACTGGTTGCCTGAACAGTCACACTTGCAACCATG 240
Db     243 TTGGTCCTGAGCTGGTTAAAAGGAACACTGGTTGCCTGAACAGTCACACTTGCAACCATG 302

Qy     241 ATGCCTAAACATTGCTTTCTAGGCTTCCTCATCAGTTTCTTCCTTACTGGTGTAGCAGGA 300
Db     303 ATGCCTAAACATTGCTTTCTAGGCTTCCTCATCAGTTTCTTCCTTACTGGTGTAGCAGGA 362

Qy     301 ACTCAGTCAACGCATGAGTCTCTGAAGCCTCAGAGGGTACAATTTCAGTCCCGAAATTTT 360
Db     363 ACTCAGTCAACGCATGAGTCTCTGAAGCCTCAGAGGGTACAATTTCAGTCCCGAAATTTT 422

Qy     361 CACAACATTTTGCAATGGCAGCCTGGGAGGGCACTTACTGGCAACAGCAGTGTCTATTTT 420
Db     423 CACAACATTTTGCAATGGCAGCCTGGGAGGGCACTTACTGGCAACAGCAGTGTCTATTTT 482

Qy     421 GTGCAGTACAAAATCATGTTCTCATGCAGCATGAAAAGCTCTCACCAGAAGCCAAGTGGA 480
Db     483 GTGCAGTACAAAAT---------------------------------------------- 496

Qy     481 TGCTGGCAGCACATTTCTTGTAACTTCCCAGGCTGCAGAACATTGGCTAAATATGGACAG 540
Db     497 ----------------------------------------------ATATGGACAG 506

Qy     541 AGACAATGGAAAAATAAAGAAGACTGTTGGGGTACTCAAGAACTCTCTTGTGACCTTACC 600
Db     507 AGACAATGGAAAAATAAAGAAGACTGTTGGGGTACTCAAGAACTCTCTTGTGACCTTACC 566

Qy     601 AGTGAAACCTCAGACATACAGGAACCTTATTACGGGAGGGTGAGGGCGGCCTCGGCTGGG 660
Db     567 AGTGAAACCTCAGACATACAGGAACCTTATTACGGGAGGGTGAGGGCGGCCTCGGCTGGG 626

Qy     661 AGCTACTCAGAATGGAGCATGACGCCGCGGTTCACTCCCTGGTGGGAAACAAAAATAGAT 720
Db     627 AGCTACTCAGAATGGAGCATGACGCCGCGGTTCACTCCCTGGTGGGAAACAAAAATAGAT 686

Qy     721 CCTCCAGTCATGAATATAACCCAAGTCAATGGCTCTTTGTTGGTAATTCTCCATGCTCCA 780
Db     687 CCTCCAGTCATGAATATAACCCAAGTCAATGGCTCTTTGTTGGTAATTCTCCATGCTCCA 746

Qy     781 AATTTACCATATAGATACCAAAAGGAAAAAAATGTATCTATAGAAGATTACTATGAACTA 840
Db     747 AATTTACCATATAGATACCAAAAGGAAAAAAATGTATCTATAGAAGATTACTATGAACTA 806

Qy     841 CTATACCGAGTTTTTATAATTAACAATTCACTAGAAAAGGAGCAAAAGGTTTATGAAGGG 900
Db     807 CTATACCGAGTTTTTATAATTAACAATTCACTAGAAAAGGAGCAAAAGGTTTATGAAGGG 866

Qy     901 GCTCACAGAGCGGTTGAAATTGAAGCTCTAACACCACACTCCAGCTACTGTGTAGTGGCT 960
Db     867 GCTCACAGAGCGGTTGAAATTGAAGCTCTAACACCACACTCCAGCTACTGTGTAGTGGCT 926

Qy     961 GAAATATATCAGCCCATGTTAGACAGAAGAAGTCAGAGAAGTGAAGAGAGATGTGTGGAA 1020
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Db     927 GAAATATATCAGCCCATGTTAGACAGAAGAAGTCAGAGAAGTGAAGAGAGATGTGTGGAA 986

Qy    1021 ATTCCATGACTTGTGGAATTTGGCATTCAGCAATGTGGAAATTCTAAAGCTCCCTGAGAA 1080
Db     987 ATTCCATGACTTGTGGAATTTGGCATTCAGCAATGTGGAAATTCTAAAGCTCCCTGAGAA 1046

Qy    1081 CAGGATGACTCGTGTTTGAAGGATCTTATTTAAAATTGTTTTTGTATTTTCTTAAAGCAA 1140
Db    1047 CAGGATGACTCGTGTTTGAAGGATCTTATTTAAAATTGTTTTTGTATTTTCTTAAAGCAA 1106

Qy    1141 TATTCACTGTTACACCTTGGGGACTTCTTTGTTTATCCATTCTTTTATCCTTTATATTTC 1200
Db    1107 TATTCACTGTTACACCTTGGGGACTTCTTTGTTTACCCATTCTTTTATCCTTTATATTTC 1166

Qy    1201 ATTTGTAAACTATATTTGAACGACATTCCCCCCGAAAAATTGAAATGTAAAGATGAGGCA 1260
Db    1167 ATTTGTAAACTATATTTGAACGACATTCCCCCCGAAAAATTGAAATGTAAAGATGAGGCA 1226

      1261 GAGAATAAAGTGTTCTATGAAAAAAAAAA 1289
Db    1227 GAGAATAAAGTGTTCTATGAAATTCAGAA 1255
```

RESULT 4
AAL46000
ID AAL46000 standard; cDNA; 1255 BP.
XX
AC AAL46000;
XX
DT 08-AUG-2002 (first entry)
XX
DE Human cytokine receptor variant 2 coding sequence.
XX
KW Human; cytokine receptor; immune disease; psoriasis; cancer; infection;
KW rheumatoid arthritis; multiple sclerosis; Crohn's disease;
KW ulcerative colitis; transplant rejection; abortion; antipsoriatic;
KW immunosuppressive; antirheumatic; antiarthritic; neuroprotective;
KW antiinflammatory; antiulcer; cytostatic; dermatological;
KW chromosome 6q24.1-25.2; receptor; gene; ss.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   304..999
FT   /*tag= a
FT   /product= "cytokine receptor variant 2"
XX
EP1191035-A2.
XX
PD 27-MAR-2002.
XX
PF 24-AUG-2001; 2001EP-0250307.
XX
PR 25-SEP-2000; 2000DE-1048626.
PR 17-NOV-2000; 2000DE-1058907.
PR 19-DEC-2000; 2000DE-1064906.
XX
PA (SCHD) SCHERING AG.
XX
PI Weiss B, Sabat R, Assadullah K, Toshi L;
XX
DR WPI; 2002-332210/37.
DR P-PSDB; AAO17381.
XX
PT New nucleic acid encoding soluble cytokine receptor, useful for
PT diagnosis and treatment of e.g. immune disease, also related protein
PT and antibodies -
XX
PS Claim 1; Page 13; 21pp; German.
XX
CC The present invention provides the protein and coding sequences of 3
CC variants of a human cytokine receptor. The sequences can be used in the
CC diagnosis, prevention and treatment of immune diseases, including
CC psoriasis, cancer, chronic/life-threatening infections, rheumatoid
CC arthritis, multiple sclerosis, Crohn's disease, ulcerative colitis and
CC transplant rejection and in reproductive medicine, e.g. for diagnosing
CC abnormal immune reactions which cause abortions. The present sequence is
CC the coding sequence of variant 2 of the invention.
XX
SQ Sequence 1255 BP; 402 A; 251 C; 246 G; 356 T; 0 other;

Query Match   81.8%; Score 1078.4; DB 24; Length 1255;
Best Local Similarity   92.4%; Pred. No. 1.6e-213;
Matches 1185; Conservative   0; Mismatches   1; Indels   96; Gaps   1;

```
Qy       1 CAGTTTCTTCATCTGTAACATCAAATGAATAATAATACCAATCTCCTAGACTTCATAAGA 60
Db      67 CAGTTTCTTCATCTGTAACATCAAATGAATAATAATACCAATCTCCTAGACTTCATAAGA 126

Qy      61 GGATTAACAAAGACAAAATATGGGAAAAACATAACATGGCGTCCCATAATTATTAGATCT 120
Db     127 GGATTAACAAAGACAAAATATGGGAAAAACATAACATGGCGTCCCATAATTATTAGATCT 186

Qy     121 TATTATTGACACTAAAATGGCATTAAAATTACCAAAAGGAAGACAGCATCTGTTTCCTCT 180
Db     187 TATTATTGACACTAAAATGGCATTAAAATTACCAAAAGGAAGACAGCATCTGTTTCCTCT 246

Qy     181 TTGGTCCTGAGCTGGTTAAAAGGAACACTGGTTGCCTGAACAGTCACACTTGCAACCATG 240
Db     247 TTGGTCCTGAGCTGGTTAAAAGGAACACTGGTTGCCTGAACAGTCACACTTGCAACCATG 306

Qy     241 ATGCCTAAACATTGCTTTCTAGGCTTCCTCATCAGTTTCTTCCTTACTGGTGTAGCAGGA 300
Db     307 ATGCCTAAACATTGCTTTCTAGGCTTCCTCATCAGTTTCTTCCTTACTGGTGTAGCAGGA 366

Qy     301 ACTCAGTCAACGCATGAGTCTCTGAAGCCTCAGAGGGTACAATTTCAGTCCCGAAATTTT 360
Db     367 ACTCAGTCAACGCATGAGTCTCTGAAGCCTCAGAGGGTACAATTTCAGTCCCGAAATTTT 426

Qy     361 CACAACATTTTGCAATGGCAGCCTGGGAGGGCACTTACTGGCAACAGCAGTGTCTATTTT 420
Db     427 CACAACATTTTGCAATGGCAGCCTGGGAGGGCACTTACTGGCAACAGCAGTGTCTATTTT 486

Qy     421 GTGCAGTACAAAATCATGTTCTCATGCAGCATGAAAAGCTCTCACCAGAAGCCAAGTGGA 480
Db     487 GTGCAGTACAAAAT---------------------------------------------- 500

Qy     481 TGCTGGCAGCACATTTCTTGTAACTTCCCAGGCTGCAGAACATTGGCTAAATATGGACAG 540
Db     501 ----------------------------------------------------ATATGGACAG 510

Qy     541 AGACAATGGAAAAATAAAGAAGACTGTTGGGGTACTCAAGAACTCTCTTGTGACCTTACC 600
Db     511 AGACAATGGAAAAATAAAGAAGACTGTTGGGGTACTCAAGAACTCTCTTGTGACCTTACC 570

Qy     601 AGTGAAACCTCAGACATACAGGAACCTTATTACGGGAGGGTGAGGGCGGCCTCGGCTGGG 660
Db     571 AGTGAAACCTCAGACATACAGGAACCTTATTACGGGAGGGTGAGGGCGGCCTCGGCTGGG 630

Qy     661 AGCTACTCAGAATGGAGCATGACGCCGCGGTTCACTCCCTGGTGGGAAACAAAAATAGAT 720
Db     631 AGCTACTCAGAATGGAGCATGACGCCGCGGTTCACTCCCTGGTGGGAAACAAAAATAGAT 690

Qy     721 CCTCCAGTCATGAATATAACCCAAGTCAATGGCTCTTTGTTGGTAATTCTCCATGCTCCA 780
Db     691 CCTCCAGTCATGAATATAACCCAAGTCAATGGCTCTTTGTTGGTAATTCTCCATGCTCCA 750

Qy     781 AATTTACCATATAGATACCAAAAGGAAAAAAAATGTATCTATAGAAGATTACTATGAACTA 840
Db     751 AATTTACCATATAGATACCAAAAGGAAAAAAAATGTATCTATAGAAGATTACTATGAACTA 810

Qy     841 CTATACCGAGTTTTTATAATTAACAATTCACTAGAAAAGGAGCAAAAGGTTTATGAAGGG 900
Db     811 CTATACCGAGTTTTTATAATTAACAATTCACTAGAAAAGGAGCAAAAGGTTTATGAAGGG 870
```

```
Qy     901 GCTCACAGAGCGGTTGAAATTGAAGCTCTAACACCACACTCCAGCTACTGTGTAGTGGCT 960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     871 GCTCACAGAGCGGTTGAAATTGAAGCTCTAACACCACACTCCAGCTACTGTGTAGTGGCT 930

Qy     961 GAAATATATCAGCCCATGTTAGACAGAAGAAGTCAGAGAAGTGAAGAGAGATGTGTGGAA 1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     931 GAAATATATCAGCCCATGTTAGACAGAAGAAGTCAGAGAAGTGAAGAGAGATGTGTGGAA 990

Qy    1021 ATTCCATGACTTGTGGAATTTGGCATTCAGCAATGTGGAAATTCTAAAGCTCCCTGAGAA 1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     991 ATTCCATGACTTGTGGAATTTGGCATTCAGCAATGTGGAAATTCTAAAGCTCCCTGAGAA 1050

Qy    1081 CAGGATGACTCGTGTTTGAAGGATCTTATTTAAAATTGTTTTTGTATTTTCTTAAAGCAA 1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1051 CAGGATGACTCGTGTTTGAAGGATCTTATTTAAAATTGTTTTTGTATTTTCTTAAAGCAA 1110

Qy    1141 TATTCACTGTTACACCTTGGGGACTTCTTTGTTTATCCATTCTTTTATCCTTTATATTTC 1200
           |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db    1111 TATTCACTGTTACACCTTGGGGACTTCTTTGTTTACCCATTCTTTTATCCTTTATATTTC 1170

Qy    1201 ATTTGTAAACTATATTTGAACGACATTCCCCCCGAAAAATTGAAATGTAAAGATGAGGCA 1260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1171 ATTTGTAAACTATATTTGAACGACATTCCCCCCGAAAAATTGAAATGTAAAGATGAGGCA 1230

Qy    1261 GAGAATAAAGTGTTCTATGAAA 1282
           |||||||||||||||||||||||
Db    1231 GAGAATAAAGTGTTCTATGAAA 1252
```

RESULT 5
ABK50076
ID ABK50076 standard; DNA; 2271 BP.
XX
AC ABK50076;
XX
DT 15-JUL-2002 (first entry)
XX
DE DNA encoding human IL-TIF/IL-22 binding protein #1.
XX
KW Human; soluble protein; interleukin-TIF/IL-22; IL-TIF/IL-22; IL-22BP;
KW IL-TIF/IL-22 antagonist; gene; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 110..805
FT /*tag= a
FT /product= "Human IL-TIF/IL-22 binding protein #1"
FT /note= "This sequence can optionally start at
FT position 113"
XX
PN WO200224912-A2.
XX
PD 28-MAR-2002.
XX
PF 21-SEP-2001; 2001WO-US29576.
XX
PR 22-SEP-2000; 2000US-234583P.
PR 03-NOV-2000; 2000US-245495P.
PR 31-JUL-2001; 2001US-0919162.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Renauld J, Dumoutier L;
XX
DR WPI; 2002-383190/41.
DR P-PSDB; AAU80000.
XX
PT Polynucleotide and polypeptide of soluble protein which binds to
PT interleukin-TIF/IL-22 useful for inhibiting effect of IL-TIF/IL-22 on a
PT cell -
XX
PS Claim 1; Page 38-39; 42pp; English.

XX
CC The present invention relates to a new polynucleotide that encodes a
CC soluble protein which binds to interleukin (IL)-TIF/IL-22 (also referred
CC to as IL-22BP), where the complementary sequence of the invention
CC hybridises under stringent conditions to a nucleotide sequence of 2271
CC or 2366 base pairs, as given in the specification. The molecules of the
CC invention are useful for inhibiting (antagonising) effect of IL-TIF/IL-22
CC on a cell, for determining whether IL-TIF/IL-22 is present in a sample,
CC for inhibiting binding of IL-TIF/IL-22 to a binding partner, preferably
CC in vitro, and for obtaining an antibody molecule specific for the soluble
CC binding protein of the invention, from a population or panel of antibody
CC molecules of diverse binding specificity. The soluble protein is further
CC useful in manufacture of a medicament for treating an IL-22 mediated
CC disease and for assaying an agent, preferably an antibody or a peptide
CC fragment of IL-TIF/IL-22 or the soluble protein, that modulates binding
CC of the soluble protein to IL-TIF/IL-22, where the agent identified is
CC used in the manufacture of medicament for treating IL-TIF/IL-22 mediated
CC disorder. The antibody is useful for determining presence of the soluble
CC protein, where the antibody is detectably labelled. The present nucleic
CC acid sequence encodes the human IL-TIF/IL-22 binding protein #1 of the
CC invention.
XX
SQ Sequence 2271 BP; 709 A; 400 C; 444 G; 718 T; 0 other;

Query Match 69.0%; Score 910; DB 24; Length 2271;
Best Local Similarity 91.0%; Pred. No. 1.1e-178;
Matches 1019; Conservative 0; Mismatches 5; Indels 96; Gaps 1;

```
Qy     170 CTGTTTCCTCTTTGGTCCTGAGCTGGTTAAAAGGAACACTGGTTGCCTGAACAGTCACAC 229
           | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      42 CAGTTTCCTCTTTGGTCCTGAGCTGGTTAAAAGGAACACTGGTTGCCTGAACAGTCACAC 101

Qy     230 TTGCAACCATGATGCCTAAACATTGCTTTCTAGGCTTCCTCATCAGTTTCTTCCTTACTG 289
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     102 TTGCAACCATGATGCCTAAACATTGCTTTCTAGGCTTCCTCATCAGTTTCTTCCTTACTG 161

Qy     290 GTGTAGCAGGAACTCAGTCAACGCATGAGTCTCTGAAGCCTCAGAGGGTACAATTTCAGT 349
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     162 GTGTAGCAGGAACTCAGTCAACGCATGAGTCTCTGAAGCCTCAGAGGGTACAATTTCAGT 221

Qy     350 CCCGAAATTTTCACAACATTTTGCAATGGCAGCCTGGGAGGGCACTTACTGGCAACAGCA 409
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     222 CCCGAAATTTTCACAACATTTTGCAATGGCAGCCTGGGAGGGCACTTACTGGCAACAGCA 281

Qy     410 GTGTCTATTTTGTGCAGTACAAAATCATGTTCTCATGCAGCATGAAAAGCTCTCACCAGA 469
           ||||||||||||||||||||||||
Db     282 GTGTCTATTTTGTGCAGTACAAAAT---------------------------------- 306

Qy     470 AGCCAAGTGGATGCTGGCAGCACATTTCTTGTAACTTCCCAGGCTGCAGAACATTGGCTA 529

Db     307 ---------------------------------------------------------- 306

Qy     530 AATATGGACAGAGACAATGGAAAAATAAAGAAGACTGTTGGGGTACTCAAGAACTCTCTT 589
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     307 -ATATGGACAGAGACAATGGAAAAATAAAGAAGACTGTTGGGGTACTCAAGAACTCTCTT 365

Qy     590 GTGACCTTACCAGTGAAACCTCAGACATACAGGAACCTTATTACGGGAGGGTGAGGGCGG 649
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     366 GTGACCTTACCAGTGAAACCTCAGACATACAGGAACCTTATTACGGGAGGGTGAGGGCGG 425

Qy     650 CCTCGGCTGGGAGCTACTCAGAATGGAGCATGACGCCGCGGTTCACTCCCTGGTGGGAAA 709
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     426 CCTCGGCTGGGAGCTACTCAGAATGGAGCATGACGCCGCGGTTCACTCCCTGGTGGGAAA 485

Qy     710 CAAAAATAGATCCTCCAGTCATGAATATAACCCAAGTCAATGGCTCTTTGTTGGTAATTC 769
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     486 CAAAAATAGATCCTCCAGTCATGAATATAACCCAAGTCAATGGCTCTTTGTTGGTAATTC 545

Qy     770 TCCATGCTCCAAATTTACCATATAGATACCAAAAGGAAAAAAATGTATCTATAGAAGATT 829
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     546 TCCATGCTCCAAATTTACCATATAGATACCAAAAGGAAAAAAATGTATCTATAGAAGATT 605

Qy     830 ACTATGAACTACTATACCGAGTTTTTATAATTAACAATTCACTAGAAAAGGAGCAAAAGG 889
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Db    606 ACTATGAACTACTATACCGAGTTTTTATAATTAACAATTCACTAGAAAAGGAGCAAAAGG 665

Qy    890 TTTATGAAGGGGCTCACAGAGCGGTTGAAATTGAAGCTCTAACACCACACTCCAGCTACT 949
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    666 TTTATGAAGGGGCTCACAGAGCGGTTGAAATTGAAGCTCTAACACCACACTCCAGCTACT 725

Qy    950 GTGTAGTGGCTGAAATATATCAGCCCATGTTAGACAGAAGAAGTCAGAGAAGTGAAGAGA 1009
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    726 GTGTAGTGGCTGAAATATATCAGCCCATGTTAGACAGAAGAAGTCAGAGAAGTGAAGAGA 785

Qy   1010 GATGTGTGGAAATTCCATGACTTGTGGAATTTGGCATTCAGCAATGTGGAAATTCTAAAG 1069
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    786 GATGTGTGGAAATTCCATGACTTGTGGAATTTGGCATTCAGCAATGTGGAAATTCTAAAG 845

Qy   1070 CTCCCTGAGAACAGGATGACTCGTGTTTGAAGGATCTTATTTAAAATTGTTTTTGTATTT 1129
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    846 CTCCCTGAGAACAGGATGACTCGTGTTTGAAGGATCTTATTTAAAATTGTTTTTGTATTT 905

Qy   1130 TCTTAAAGCAATATTCACTGTTACACCTTGGGGACTTCTTTGTTTATCCATTCTTTTATC 1189
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    906 TCTTAAAGCAATATTCACTGTTACACCTTGGGGACTTCTTTGTTTATCCATTCTTTTATC 965

Qy   1190 CTTTATATTTCATTTGTAAACTATATTTGAACGACATTCCCCCCGAAAAATTGAAATGTA 1249
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    966 CTTTATATTTCATTTGTAAACTATATTTGAACGACATTCCCCCCGAAAAATTGAAATGTA 1025

Qy   1250 AAGATGAGGCAGAGAATAAAGTGTTCTATGAAAAAAAAAA 1289
          ||||||||||||||||||||||||||||||||   | ||
Db   1026 AAGATGAGGCAGAGAATAAAGTGTTCTATGAAATTCAGAA 1065
```

RESULT 6
AAD09745
ID AAD09745 standard; cDNA; 2149 BP.
XX
AC AAD09745;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human ZCYTO18 soluble receptor antagonist cDNA, zcytor16.
XX
KW Human; cytostatic; cytokine; ZCYTO18 protein; genetic abnormality;
KW cancer; inflammation; gene therapy; zcytor16; ss.
XX
OS Homo sapiens.
XX

Key	Location/Qualifiers
CDS	1..696
	/*tag= a
FT	/product= "Human zcytor16 protein"

XX
PN WO200146422-A1.
XX
PD 28-JUN-2001.
XX
PF 22-DEC-2000; 2000WO-US35308.
XX
PR 23-DEC-1999; 99US-0471767.
PR 01-DEC-2000; 2000US-0250841.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Presnell SR, Kindsvogel W;
XX
DR WPI; 2001-408648/43.
DR P-PSDB; AAE05048.
XX
PT Novel human cytokine polypeptide, ZCYTO18, useful for treating cancer -
XX
PS Example 13A; Page 156-158; 167pp; English.
XX
CC The patent discloses novel human cytokine, ZCYTO18 protein and its
CC corresponding DNA. ZCYTO18 protein induces proliferation of cells
CC expressing zcytor11, a receptor for ZCYTO18 or induces cytotoxicity
CC in K5626 cells. ZCYTO18 DNA is useful for detecting a genetic
CC abnormality in a patient. ZCYTO18 DNA and its antibodies are useful
CC for detecting cancer and inflammation. ZCYTO18 protein is useful for
CC killing cancer cells. It is useful for increasing platelets in a
CC patient or injured tissue. It is also used in gene therapy.
CC The present sequence is a cDNA encoding human zcytor16, which is a
CC naturally expressed soluble receptor antagonist of ZCYTO18 protein.
XX
SQ Sequence 2149 BP; 685 A; 381 C; 421 G; 662 T; 0 other;

Query Match 63.1%; Score 831.6; DB 22; Length 2149;
Best Local Similarity 90.4%; Pred. No. 1.8e-162;
Matches 951; Conservative 0; Mismatches 4; Indels 97; Gaps 2;

```
Qy    238 ATGATGCCTAAACATTGCTTTCTAGGCTTCCTCATCAGTTTCTTCCTTACTGGTGTAGCA 297
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGATGCCTAAACATTGCTTTCTAGGCTTCCTCATCAGTTTCTTCCTTACTGGTGTAGCA 60

Qy    298 GGAACTCAGTCAACGCATGAGTCTCTGAAGCCTCAGAGGGTACAATTTCAGTCCCGAAAT 357
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GGAACTCAGTCAACGCATGAGTCTCTGAAGCCTCAGAGGGTACAATTTCAGTCCCGAAAT 120

Qy    358 TTTCACAACATTTTGCAATGGCAGCCTGGGAGGGCACTTACTGGCAACAGCAGTGTCTAT 417
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 TTTCACAACATTTTGCAATGGCAGCCTGGGAGGGCACTTACTGGCAACAGCAGTGTCTAT 180

Qy    418 TTTGTGCAGTACAAAATCATGTTCTCATGCAGCATGAAAAGCTCTCACCAGAAGCCAAGT 477
          ||||||||||||||||
Db    181 TTTGTGCAGTACAAAAT---------------------------------------- 197

Qy    478 GGATGCTGGCAGCACATTTCTTGTAACTTCCCAGGCTGCAGAACATTGGCTAAATATGGA 537
                                                          |||||||
Db    198 ----------------------------------------------------ATATGGA 204

Qy    538 CAGAGACAATGGAAAAATAAAGAAGACTGTTGGGGTACTCAAGAACTCTCTTGTGACCTT 597
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    205 CAGAGACAATGGAAAAATAAAGAAGACTGTTGGGGTACTCAAGAACTCTCTTGTGACCTT 264

Qy    598 ACCAGTGAAACCTCAGACATACAGGAACCTTATTACGGGAGGGTGAGGGCGGCCTCGGCT 657
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    265 ACCAGTGAAACCTCAGACATACAGGAACCTTATTACGGGAGGGTGAGGGCGGCCTCGGCT 324

Qy    658 GGGAGCTACTCAGAATGGAGCATGACGCCGCGGTTCACTCCCTGGTGGGAAACAAAAATA 717
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    325 GGGAGCTACTCAGAATGGAGCATGACGCCGCGGTTCACTCCCTGGTGGGAAACAAAAATA 384

Qy    718 GATCCTCCAGTCATGAATATAACCCAAGTCAATGGCTCTTTGTTGGTAATTCTCCATGCT 777
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    385 GATCCTCCAGTCATGAATATAACCCAAGTCAATGGCTCTTTGTTGGTAATTCTCCATGCT 444

Qy    778 CCAAATTTACCATATAGATACCAAAAGGAAAAAAATGTATCTATAGAAGATTACTATGAA 837
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    445 CCAAATTTACCATATAGATACCAAAAGGAAAAAAATGTATCTATAGAAGATTACTATGAA 504

Qy    838 CTACTATACCGAGTTTTTATAATTAACAATTCACTAGAAAAGGAGCAAAAGGTTTATGAA 897
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    505 CTACTATACCGAGTTTTTATAATTAACAATTCACTAGAAAAGGAGCAAAAGGTTTATGAA 564

Qy    898 GGGGCTCACAGAGCGGTTGAAATTGAAGCTCTAACACCACACTCCAGCTACTGTGTAGTG 957
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    565 GGGGCTCACAGAGCGGTTGAAATTGAAGCTCTAACACCACACTCCAGCTACTGTGTAGTG 624

Qy    958 GCTGAAATATATCAGCCCATGTTAGACAGAAGAAGTCAGAGAAGTGAAGAGAGATGTGTG 1017
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    625 GCTGAAATATATCAGCCCATGTTAGACAGAAGAAGTCAGAGAAGTGAAGAGAGATGTGTG 684

Qy   1018 GAAATTCCATGACTTGTGGAATTTGGCATTCAGCAATGTGGAAATTCTAAAGCTCCCTGA 1077
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    685 GAAATTCCATGACTTGTGGAATTTGGCATTCAGCAATGTGGAAATTCTAAAGCTCCCTGA 744

Qy   1078 GAACAGGATGACTCGTGTTTGAAGGATCTTATTTAAAATTGTTTTTGTATTTTCTTAAAG 1137
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     745 GAACAGGATGACTCGTGTTTGAAGGATCTTATTTAAAATTGTTTTTGTATTTTCTTAAAG 804

Qy    1138 CAATATTCACTGTTACACCTTGGGGACTTCTTTGTTTATCCATTCTTTTATCCTTTATAT 1197
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     805 CAATATTCACTGTTACACCTTGGGGACTTCTTTGTTTATCCATTCTTTTATCCTTTATAT 864

Qy    1198 TTCATTTGTAAACTATATTTGAACGACATTCCCCCCGAAAAATTGAAATGTAAAGATGAG 1257
          ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     865 TTCATTT-TAAACTATATTTGAACGACATTCCCCCCGAAAAATTGAAATGTAAAGATGAG 923

Qy    1258 GCAGAGAATAAAGTGTTCTATGAAAAAAAAAA 1289
          |||||||||||||||||||||||||    | ||
Db     924 GCAGAGAATAAAGTGTTCTATGAAATTCAGAA 955
```

RESULT 7
AAF83735
ID AAF83735 standard; cDNA; 2149 BP.
[redacted] AAF83735;
DT 23-JUL-2001 (first entry)
XX
DE Human cytokine receptor, zcytor16 encoding cDNA.
XX
KW Cytokine receptor; zcytor16; IL-TIF; antiinflammatory; cytostatic;
KW antirheumatic; antiarthritic; antiasthmatic; antiatherosclerotic;
KW immunosuppressive; chromosome 6q24.1-25.2; human; ss.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   1..696
FT   /*tag= a
FT   /product= "zcytor16"
XX
PN WO200140467-A1.
XX
PD 07-JUN-2001.
XX
PF 01-DEC-2000; 2000WO-US32703.
XX
PR 03-DEC-1999;   99US-0169049.
PR 13-SEP-2000; 2000US-0232219.
PR 31-OCT-2000; 2000US-0244610.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
[redacted] Presnell SR, Xu W, Kindsvogel W, Chen Z;
XX
DR WPI; 2001-356158/37.
DR P-PSDB; AAB62657.
XX
PT New soluble cytokine receptor polypeptides and polynucleotides, useful
PT for diagnosing and treating cancer and inflammatory conditions -
XX
PS Claim 10; Page 186-188; 210pp; English.
XX
CC The invention relates to a human cytokine receptor polypeptide,
CC designated zcytor16. The zcytor16 polypeptide can be expressed by
CC standard recombinant methodology and can bind to IL-TIF (undefined). The
CC zcytor16 protein is useful for: inhibiting IL-TIF induced proliferation
CC or differentiation of hematopoietic cell(s) (progenitors); reducing
CC IL-TIF induced or IL-9 induced inflammation; and suppressing an
CC inflammatory response in a mammal with inflammation. Heteromeric/
CC multimeric receptor polypeptides such as soluble zcytor 16/CRF2-4 can be
CC used to reduce progression and symptoms of cancer. Zcytor16 polypeptides
CC can also be used to detect IL-TIF levels which is indicative of
CC pathological conditions including inflammatory states (e.g. rheumatoid
CC arthritis) and cancer. Antibodies that bind zcytor16 polypeptides and the
CC polypeptides themselves are useful for the treatment of inflammation,
CC inflammatory diseases (e.g. infection, asthma, inflammatory bowel
CC disease, rheumatoid arthritis and atherosclerosis) and autoimmune
CC diseases. The antibodies and zcytor16 polynucleotides are also useful
CC for detecting cancer. The present sequence represents a cDNA encoding
CC the human zcytor16 protein.
XX
SQ Sequence 2149 BP; 685 A; 381 C; 421 G; 662 T; 0 other;

Query Match 63.1%; Score 831.6; DB 22; Length 2149;
Best Local Similarity 90.4%; Pred. No. 1.8e-162;
Matches 951; Conservative 0; Mismatches 4; Indels 97; Gaps 2;

```
Qy     238 ATGATGCCTAAACATTGCTTTCTAGGCTTCCTCATCAGTTTCTTCCTTACTGGTGTAGCA 297
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 ATGATGCCTAAACATTGCTTTCTAGGCTTCCTCATCAGTTTCTTCCTTACTGGTGTAGCA 60

Qy     298 GGAACTCAGTCAACGCATGAGTCTCTGAAGCCTCAGAGGGTACAATTTCAGTCCCGAAAT 357
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 GGAACTCAGTCAACGCATGAGTCTCTGAAGCCTCAGAGGGTACAATTTCAGTCCCGAAAT 120

Qy     358 TTTCACAACATTTTGCAATGGCAGCCTGGGAGGGCACTTACTGGCAACAGCAGTGTCTAT 417
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 TTTCACAACATTTTGCAATGGCAGCCTGGGAGGGCACTTACTGGCAACAGCAGTGTCTAT 180

Qy     418 TTTGTGCAGTACAAAATCATGTTCTCATGCAGCATGAAAAGCTCTCACCAGAAGCCAAGT 477
           ||||||||||||||||
Db     181 TTTGTGCAGTACAAAAT---------------------------------------------- 197

Qy     478 GGATGCTGGCAGCACATTTCTTGTAACTTCCCAGGCTGCAGAACATTGGCTAAATATGGA 537
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Db     198 ----------------------------------------------------------ATATGGA 204

Qy     538 CAGAGACAATGGAAAAATAAAGAAGACTGTTGGGGTACTCAAGAACTCTCTTGTGACCTT 597
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     205 CAGAGACAATGGAAAAATAAAGAAGACTGTTGGGGTACTCAAGAACTCTCTTGTGACCTT 264

Qy     598 ACCAGTGAAACCTCAGACATACAGGAACCTTATTACGGGAGGGTGAGGGCGGCCTCGGCT 657
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     265 ACCAGTGAAACCTCAGACATACAGGAACCTTATTACGGGAGGGTGAGGGCGGCCTCGGCT 324

Qy     658 GGGAGCTACTCAGAATGGAGCATGACGCCGCGGTTCACTCCCTGGTGGGAAACAAAAATA 717
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     325 GGGAGCTACTCAGAATGGAGCATGACGCCGCGGTTCACTCCCTGGTGGGAAACAAAAATA 384

Qy     718 GATCCTCCAGTCATGAATATAACCCAAGTCAATGGCTCTTTGTTGGTAATTCTCCATGCT 777
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     385 GATCCTCCAGTCATGAATATAACCCAAGTCAATGGCTCTTTGTTGGTAATTCTCCATGCT 444

Qy     778 CCAAATTTACCATATAGATACCAAAAGGAAAAAAATGTATCTATAGAAGATTACTATGAA 837
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     445 CCAAATTTACCATATAGATACCAAAAGGAAAAAAATGTATCTATAGAAGATTACTATGAA 504

Qy     838 CTACTATACCGAGTTTTTATAATTAACAATTCACTAGAAAAGGAGCAAAAGGTTTATGAA 897
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     505 CTACTATACCGAGTTTTTATAATTAACAATTCACTAGAAAAGGAGCAAAAGGTTTATGAA 564

Qy     898 GGGGCTCACAGAGCGGTTGAAATTGAAGCTCTAACACCACACTCCAGCTACTGTGTAGTG 957
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     565 GGGGCTCACAGAGCGGTTGAAATTGAAGCTCTAACACCACACTCCAGCTACTGTGTAGTG 624

Qy     958 GCTGAAATATATCAGCCCATGTTAGACAGAAGAAGTCAGAGAAGTGAAGAGAGATGTGTG 1017
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     625 GCTGAAATATATCAGCCCATGTTAGACAGAAGAAGTCAGAGAAGTGAAGAGAGATGTGTG 684

Qy    1018 GAAATTCCATGACTTGTGGAATTTGGCATTCAGCAATGTGGAAATTCTAAAGCTCCCTGA 1077
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     685 GAAATTCCATGACTTGTGGAATTTGGCATTCAGCAATGTGGAAATTCTAAAGCTCCCTGA 744

Qy    1078 GAACAGGATGACTCGTGTTTGAAGGATCTTATTTAAAATTGTTTTTGTATTTTCTTAAAG 1137
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     745 GAACAGGATGACTCGTGTTTGAAGGATCTTATTTAAAATTGTTTTTGTATTTTCTTAAAG 804

Qy    1138 CAATATTCACTGTTACACCTTGGGGACTTCTTTGTTTATCCATTCTTTTATCCTTTATAT 1197
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db     805 CAATATTCACTGTTACACCTTGGGGACTTCTTTGTTTATCCATTCTTTTATCCTTTATAT 864

Qy    1198 TTCATTTGTAAACTATATTTGAACGACATTCCCCCCGAAAAATTGAAATGTAAAGATGAG 1257
           ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     865 TTCATTT-TAAACTATATTTGAACGACATTCCCCCCGAAAAATTGAAATGTAAAGATGAG 923

Qy    1258 GCAGAGAATAAAGTGTTCTATGAAAAAAAAAA 1289
           |||||||||||||||||||||||||    | ||
Db     924 GCAGAGAATAAAGTGTTCTATGAAATTCAGAA 955
```

RESULT 8
AAL46001
ID AAL46001 standard; cDNA; 810 BP.
XX
AC AAL46001;
XX
DT 08-AUG-2002 (first entry)
XX
[redacted] Human cytokine receptor variant 3 coding sequence.

KW Human; cytokine receptor; immune disease; psoriasis; cancer; infection;
KW rheumatoid arthritis; multiple sclerosis; Crohn's disease;
KW ulcerative colitis; transplant rejection; abortion; antipsoriatic;
KW immunosuppressive; antirheumatic; antiarthritic; neuroprotective;
KW antiinflammatory; antiulcer; cytostatic; dermatological;
KW chromosome 6q24.1-25.2; receptor; gene; ss.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   12..803
FT   /*tag= a
FT   /product= "cytokine receptor variant 3"
XX
PN EP1191035-A2.
XX
PD 27-MAR-2002.
XX
PF 24-AUG-2001; 2001EP-0250307.
XX
PR 25-SEP-2000; 2000DE-1048626.
PR 17-NOV-2000; 2000DE-1058907.
PR 19-DEC-2000; 2000DE-1064906.
XX
PA (SCHD) SCHERING AG.
XX
[redacted] Weiss B, Sabat R, Assadullah K, Toshi L;

DR WPI; 2002-332210/37.
DR P-PSDB; AAO17382.
XX
PT New nucleic acid encoding soluble cytokine receptor, useful for
PT diagnosis and treatment of e.g. immune disease, also related protein
PT and antibodies -
XX
PS Claim 1; Page 14-15; 21pp; German.
XX
CC The present invention provides the protein and coding sequences of 3
CC variants of a human cytokine receptor. The sequences can be used in the
CC diagnosis, prevention and treatment of immune diseases, including
CC psoriasis, cancer, chronic/life-threatening infections, rheumatoid
CC arthritis, multiple sclerosis, Crohn's disease, ulcerative colitis and
CC transplant rejection and in reproductive medicine, e.g. for diagnosing
CC abnormal immune reactions which cause abortions. The present sequence is
CC the coding sequence of variant 3 of the invention.
XX
SQ Sequence 810 BP; 253 A; 172 C; 184 G; 201 T; 0 other;

Query Match   61.1%; Score 805.2; DB 24; Length 810;
Best Local Similarity   99.6%; Pred. No. 4.1e-157;
Matches 807; Conservative   0; Mismatches   3; Indels   0; Gaps   0;

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Qy     227 CACTTGCAACCATGATGCCTAAACATTGCTTTCTAGGCTTCCTCATCAGTTTCTTCCTTA 286
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 CACTTGCAACCATGATGCCTAAACATTGCTTTCTAGGCTTCCTCATCAGTTTCTTCCTTA 60

Qy     287 CTGGTGTAGCAGGAACTCAGTCAACGCATGAGTCTCTGAAGCCTCAGAGGGTACAATTTC 346
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 CTGGTGTAGCAGGAACTCAGTCAACGCATGAGTCTCTGAAGCCTCAGAGGGTACAATTTC 120

Qy     347 AGTCCCGAAATTTTCACAACATTTTGCAATGGCAGCCTGGGAGGGCACTTACTGGCAACA 406
           |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db     121 AGTCCCGAAATTTTCACAACATTTTGCAATGGCAGCCGGGGAGGGCACTTACTGGCAACA 180

Qy     407 GCAGTGTCTATTTTGTGCAGTACAAAATCATGTTCTCATGCAGCATGAAAAGCTCTCACC 466
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 GCAGTGTCTATTTTGTGCAGTACAAAATCATGTTCTCATGCAGCATGAAAAGCTCTCACC 240

Qy     467 AGAAGCCAAGTGGATGCTGGCAGCACATTTCTTGTAACTTCCCAGGCTGCAGAACATTGG 526
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 AGAAGCCAAGTGGATGCTGGCAGCACATTTCTTGTAACTTCCCAGGCTGCAGAACATTGG 300

Qy     527 CTAAATATGGACAGAGACAATGGAAAAATAAAGAAGACTGTTGGGGTACTCAAGAACTCT 586
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 CTAAATATGGACAGAGACAATGGAAAAATAAAGAAGACTGTTGGGGTACTCAAGAACTCT 360

Qy     587 CTTGTGACCTTACCAGTGAAACCTCAGACATACAGGAACCTTATTACGGGAGGGTGAGGG 646
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Db     361 CTTGTGACCTTACCAGTGAAACCTCAGACATACAGGAACCTTATTACGGGAGGGTGAGGG 420

Qy     647 CGGCCTCGGCTGGGAGCTACTCAGAATGGAGCATGACGCCGCGGTTCACTCCCTGGTGGG 706
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 CGGCCTCGGCTGGGAGCTACTCAGAATGGAGCATGACGCCGCGGTTCACTCCCTGGTGGG 480

Qy     707 AAACAAAAATAGATCCTCCAGTCATGAATATAACCCAAGTCAATGGCTCTTTGTTGGTAA 766
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 AAACAAAAATAGATCCTCCAGTCATGAATATAACCCAAGTCAATGGCTCTTTGTTGGTAA 540

Qy     767 TTCTCCATGCTCCAAATTTACCATATAGATACCAAAAGGAAAAAAATGTATCTATAGAAG 826
           |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 TTCTCCATGCCCCAAATTTACCATATAGATACCAAAAGGAAAAAAATGTATCTATAGAAG 600

Qy     827 ATTACTATGAACTACTATACCGAGTTTTTATAATTAACAATTCACTAGAAAAGGAGCAAA 886
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 ATTACTATGAACTACTATACCGAGTTTTTATAATTAACAATTCACTAGAAAAGGAGCAAA 660

Qy     887 AGGTTTATGAAGGGGCTCACAGAGCGGTTGAAATTGAAGCTCTAACACCACACTCCAGCT 946
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 AGGTTTATGAAGGGGCTCACAGAGCGGTTGAAATTGAAGCTCTAACACCACACTCCAGCT 720

Qy     947 ACTGTGTAGTGGCTGAAATATATCAGCCCATGTTAGACAGAAGAAGTCAGAGAAGTGAAG 1006
           |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db     721 ACTGTGTAGTGGCTGAAATATATCAGCCCATGTTAGACAGAAGAAGTCGGAGAAGTGAAG 780

Qy    1007 AGAGATGTGTGGAAATTCCATGACTTGTGG 1036
           |||||||||||||||||||||||||||||
Db     781 AGAGATGTGTGGAAATTCCATGACTTGTGG 810
```

RESULT 9
AAD27816
ID AAD27816 standard; DNA; 792 BP.
XX
AC AAD27816;
XX
DT 18-APR-2002 (first entry)
XX
DE Human cytokine receptor gene, sbg456548CytoRa #3.
XX
KW Human; therapy; wound healing disorder; vaccine; cancer; infection;
KW autoimmune disorder; haematopoietic disorder; inflammation; arthritis;
KW Parkinson's disease; Huntington's chorea; schizophrenia; antiarrhythmic;
KW multiple sclerosis; Alzheimer's disease; analgesic; cardiant; asthma;
KW ischaemia; stroke; AIDS; bone disease; atherosclerosis; brain disorder;
KW depression; cardiovascular disease; myocardial infarction; renal failure;

KW respiratory disease; liver disorder; Fanconi's syndrome; spleen disorder;
KW type II diabetes mellitus; skeletal muscle disorder; immunosuppressive;
KW hypersplenism; renal disease; hypoglycaemia; gastrointestinal disease;
KW nootropic; cirrhosis; Hodgkin's disease; neuroleptic; antiinflammatory;
KW haemostatic; vulnerary; anticonvulsant; antirheumatic; neuroprotective;
KW nephrotropic; hypotensive; vasotropic; cytostatic; cerebroprotective;
KW allergy; cytokine receptor; gene; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..792
FT /*tag= a
FT /product= "Human cytokine receptor"
XX
PN WO200198342-A1.
XX
PD 27-DEC-2001.
XX
[redacted]
22-JUN-2001; 2001WO-US19929.
[redacted]
22-JUN-2000; 2000US-213156P.
PR 22-JUN-2000; 2000US-213161P.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PA (GLAX) GLAXO GROUP LTD.
XX
PI Agarwal P, Cogswell JP, Kabnic KS, Lai Y, Martensen SA;
PI Murdock PR, Smith RF, Strum JC, Xiang Z, Xie Q, Rizni SK;
XX
DR WPI; 2002-139783/18.
DR P-PSDB; AAE17321.
XX
PT Novel secreted and membrane-associated polypeptides and polynucleotides
PT useful for preventing, ameliorating or correcting dysfunction or
PT disease including diabetes, cancer, hypertension and growth
PT abnormalities -
XX
PS Claim 2; Page 98; 138pp; English.
XX
CC The invention relates to secreted and membrane-associated polypeptides
CC and polynucleotides. The sequences of the invention are useful in
CC diagnostic assays for detecting diseases associated with inappropriate
CC activity or levels of these polynucleotides, and in identifying their
CC agonists and antagonists that are potentially useful in therapy. The
CC sequences of the invention are useful as vaccines for inducing
CC immunological response. The sequences of the invention are useful for
[redacted] treating cancers, infections, autoimmune disorders, haematopoietic
CC disorders, wound healing disorders, cholesteryl ester storage disease,
CC inflammation, congenital muscular dystrophy, junctional epidermolysis
CC bullosa, Parkinson's disease, Huntington's chorea, multiple sclerosis,
CC viral and bacterial infections, Alzheimer's disease, asthma, arthritis,
CC allergies, schizophrenia, sbg442445PROa-associated disorders,
CC septicaemia, psoriasis, inflammatory bowel disease, transplant rejection,
CC graft verse host disease, ischaemia, stroke, acute respiratory disease
CC syndrome, restenosis, brain injury, AIDS, bone diseases, atherosclerosis,
CC brain disorders including parasupranuclear palsy, myotonic dystrophy,
CC depression, anxiety disorders and sleep disorders, cardiovascular
CC diseases including congestive heart failure and myocardial infarction,
CC respiratory diseases including chronic obstructive pulmonary disease,
CC acute bronchitis and adult respiratory distress syndrome, liver disorders
CC including hypercholesterolaemia, hypertriglyceridaemia, cirrhosis, viral
CC and non-viral hepatitis, type II diabetes mellitus, renal disease
CC including acute and chronic renal failure, glomerulonephritis, Fanconi's
CC syndrome, cystinuria, skeletal muscle disorders including hypoglycaemia
CC and tendinitis, gastrointestinal diseases including intestinal
CC obstruction and tropical sprue, spleen disorders including hypersplenism,
CC Hodgkin's disease and malignant lymphoma, testicular cancer, male
CC reproductive diseases including low testosterone and male infertility.
CC The present sequence is human cytokine receptor gene.
XX
SQ Sequence 792 BP; 251 A; 165 C; 178 G; 198 T; 0 other;

Query Match 60.1%; Score 792; DB 24; Length 792;
Best Local Similarity 100.0%; Pred. No. 2.2e-154;
Matches 792; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    238 ATGATGCCTAAACATTGCTTTCTAGGCTTCCTCATCAGTTTCTTCCTTACTGGTGTAGCA 297
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Db      1 ATGATGCCTAAACATTGCTTTCTAGGCTTCCTCATCAGTTTCTTCCTTACTGGTGTAGCA 60

Qy    298 GGAACTCAGTCAACGCATGAGTCTCTGAAGCCTCAGAGGGTACAATTTCAGTCCCGAAAT 357
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Db     61 GGAACTCAGTCAACGCATGAGTCTCTGAAGCCTCAGAGGGTACAATTTCAGTCCCGAAAT 120

Qy    358 TTTCACAACATTTTGCAATGGCAGCCTGGGAGGGCACTTACTGGCAACAGCAGTGTCTAT 417
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Db    121 TTTCACAACATTTTGCAATGGCAGCCTGGGAGGGCACTTACTGGCAACAGCAGTGTCTAT 180

Qy    418 TTTGTGCAGTACAAAATCATGTTCTCATGCAGCATGAAAAGCTCTCACCAGAAGCCAAGT 477
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Db    181 TTTGTGCAGTACAAAATCATGTTCTCATGCAGCATGAAAAGCTCTCACCAGAAGCCAAGT 240

Qy    478 GGATGCTGGCAGCACATTTCTTGTAACTTCCCAGGCTGCAGAACATTGGCTAAATATGGA 537
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GGATGCTGGCAGCACATTTCTTGTAACTTCCCAGGCTGCAGAACATTGGCTAAATATGGA 300

Qy    538 CAGAGACAATGGAAAAATAAAGAAGACTGTTGGGGTACTCAAGAACTCTCTTGTGACCTT 597
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CAGAGACAATGGAAAAATAAAGAAGACTGTTGGGGTACTCAAGAACTCTCTTGTGACCTT 360

Qy    598 ACCAGTGAAACCTCAGACATACAGGAACCTTATTACGGGAGGGTGAGGGCGGCCTCGGCT 657
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 ACCAGTGAAACCTCAGACATACAGGAACCTTATTACGGGAGGGTGAGGGCGGCCTCGGCT 420

Qy    658 GGGAGCTACTCAGAATGGAGCATGACGCCGCGGTTCACTCCCTGGTGGGAAACAAAAATA 717
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GGGAGCTACTCAGAATGGAGCATGACGCCGCGGTTCACTCCCTGGTGGGAAACAAAAATA 480

Qy    718 GATCCTCCAGTCATGAATATAACCCAAGTCAATGGCTCTTTGTTGGTAATTCTCCATGCT 777
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GATCCTCCAGTCATGAATATAACCCAAGTCAATGGCTCTTTGTTGGTAATTCTCCATGCT 540

Qy    778 CCAAATTTACCATATAGATACCAAAAGGAAAAAAATGTATCTATAGAAGATTACTATGAA 837
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 CCAAATTTACCATATAGATACCAAAAGGAAAAAAATGTATCTATAGAAGATTACTATGAA 600

Qy    838 CTACTATACCGAGTTTTTATAATTAACAATTCACTAGAAAAGGAGCAAAAGGTTTATGAA 897
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 CTACTATACCGAGTTTTTATAATTAACAATTCACTAGAAAAGGAGCAAAAGGTTTATGAA 660

Qy    898 GGGGCTCACAGAGCGGTTGAAATTGAAGCTCTAACACCACACTCCAGCTACTGTGTAGTG 957
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 GGGGCTCACAGAGCGGTTGAAATTGAAGCTCTAACACCACACTCCAGCTACTGTGTAGTG 720

Qy    958 GCTGAAATATATCAGCCCATGTTAGACAGAAGAAGTCAGAGAAGTGAAGAGAGATGTGTG 1017
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 GCTGAAATATATCAGCCCATGTTAGACAGAAGAAGTCAGAGAAGTGAAGAGAGATGTGTG 780

Qy   1018 GAAATTCCATGA 1029
          ||||||||||||
Db    781 GAAATTCCATGA 792
```

RESULT 10
AAD27815
ID AAD27815 standard; DNA; 696 BP.
XX
AC AAD27815;
XX
DT 18-APR-2002 (first entry)
XX
DE Human cytokine receptor gene, sbg456548CytoRa #2.
XX
KW Human; therapy; wound healing disorder; vaccine; cancer; infection;

KW autoimmune disorder; haematopoietic disorder; inflammation; arthritis;
KW Parkinson's disease; Huntington's chorea; schizophrenia; antiarrhythmic;
KW multiple sclerosis; Alzheimer's disease; analgesic; cardiant; asthma;
KW ischaemia; stroke; AIDS; bone disease; atherosclerosis; brain disorder;
KW depression; cardiovascular disease; myocardial infarction; renal failure;
KW respiratory disease; liver disorder; Fanconi's syndrome; spleen disorder;
KW type II diabetes mellitus; skeletal muscle disorder; immunosuppressive;
KW hypersplenism; renal disease; hypoglycaemia; gastrointestinal disease;
KW nootropic; cirrhosis; Hodgkin's disease; neuroleptic; antiinflammatory;
KW haemostatic; vulnerary; anticonvulsant; antirheumatic; neuroprotective;
KW nephrotropic; hypotensive; vasotropic; cytostatic; cerebroprotective;
KW allergy; cytokine receptor; gene; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..696
FT /*tag= a
FT /product= "Human cytokine receptor"

WO200198342-A1.

PD 27-DEC-2001.
XX
PF 22-JUN-2001; 2001WO-US19929.
XX
PR 22-JUN-2000; 2000US-213156P.
PR 22-JUN-2000; 2000US-213161P.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PA (GLAX) GLAXO GROUP LTD.
XX
PI Agarwal P, Cogswell JP, Kabnic KS, Lai Y, Martensen SA;
PI Murdock PR, Smith RF, Strum JC, Xiang Z, Xie Q, Rizni SK;
XX
DR WPI; 2002-139783/18.
DR P-PSDB; AAE17320.
XX
PT Novel secreted and membrane-associated polypeptides and polynucleotides
PT useful for preventing, ameliorating or correcting dysfunction or
PT disease including diabetes, cancer, hypertension and growth
PT abnormalities -
XX
PS Claim 2; Page 98; 138pp; English.
XX
CC The invention relates to secreted and membrane-associated polypeptides
CC and polynucleotides. The sequences of the invention are useful in
CC diagnostic assays for detecting diseases associated with inappropriate
CC activity or levels of these polynucleotides, and in identifying their
CC agonists and antagonists that are potentially useful in therapy. The
CC sequences of the invention are useful as vaccines for inducing
CC immunological response. The sequences of the invention are useful for
CC treating cancers, infections, autoimmune disorders, haematopoietic
CC disorders, wound healing disorders, cholesteryl ester storage disease,
CC inflammation, congenital muscular dystrophy, junctional epidermolysis
CC bullosa, Parkinson's disease, Huntington's chorea, multiple sclerosis,
CC viral and bacterial infections, Alzheimer's disease, asthma, arthritis,
CC allergies, schizophrenia, sbg442445PROa-associated disorders,
CC septicaemia, psoriasis, inflammatory bowel disease, transplant rejection,
CC graft verse host disease, ischaemia, stroke, acute respiratory disease
CC syndrome, restenosis, brain injury, AIDS, bone diseases, atherosclerosis,
CC brain disorders including parasupranuclear palsy, myotonic dystrophy,
CC depression, anxiety disorders and sleep disorders, cardiovascular
CC diseases including congestive heart failure and myocardial infarction,
CC respiratory diseases including chronic obstructive pulmonary disease,
CC acute bronchitis and adult respiratory distress syndrome, liver disorders
CC including hypercholesterolaemia, hypertriglyceridaemia, cirrhosis, viral
CC and non-viral hepatitis, type II diabetes mellitus, renal disease
CC including acute and chronic renal failure, glomerulonephritis, Fanconi's
CC syndrome, cystinuria, skeletal muscle disorders including hypoglycaemia
CC and tendinitis, gastrointestinal diseases including intestinal
CC obstruction and tropical sprue, spleen disorders including hypersplenism,
CC Hodgkin's disease and malignant lymphoma, testicular cancer, male
CC reproductive diseases including low testosterone and male infertility.
CC The present sequence is human cytokine receptor gene.
XX
SQ Sequence 696 BP; 224 A; 140 C; 157 G; 175 T; 0 other;

Query Match 44.8%; Score 590; DB 24; Length 696;
Best Local Similarity 87.9%; Pred. No. 1.2e-112;
Matches 696; Conservative 0; Mismatches 0; Indels 96; Gaps 1;

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Qy    238 ATGATGCCTAAACATTGCTTTCTAGGCTTCCTCATCAGTTTCTTCCTTACTGGTGTAGCA 297
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGATGCCTAAACATTGCTTTCTAGGCTTCCTCATCAGTTTCTTCCTTACTGGTGTAGCA 60

Qy    298 GGAACTCAGTCAACGCATGAGTCTCTGAAGCCTCAGAGGGTACAATTTCAGTCCCGAAAT 357
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GGAACTCAGTCAACGCATGAGTCTCTGAAGCCTCAGAGGGTACAATTTCAGTCCCGAAAT 120

Qy    358 TTTCACAACATTTTGCAATGGCAGCCTGGGAGGGCACTTACTGGCAACAGCAGTGTCTAT 417
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 TTTCACAACATTTTGCAATGGCAGCCTGGGAGGGCACTTACTGGCAACAGCAGTGTCTAT 180

Qy    418 TTTGTGCAGTACAAAATCATGTTCTCATGCAGCATGAAAAGCTCTCACCAGAAGCCAAGT 477
          ||||||||||||||||
Db    181 TTTGTGCAGTACAAAAT---------------------------------------- 197

Qy    478 GGATGCTGGCAGCACATTTCTTGTAACTTCCCAGGCTGCAGAACATTGGCTAAATATGGA 537
                                                                |||||||
Db    198 ----------------------------------------------------ATATGGA 204

Qy    538 CAGAGACAATGGAAAAATAAAGAAGACTGTTGGGGTACTCAAGAACTCTCTTGTGACCTT 597
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    205 CAGAGACAATGGAAAAATAAAGAAGACTGTTGGGGTACTCAAGAACTCTCTTGTGACCTT 264

Qy    598 ACCAGTGAAACCTCAGACATACAGGAACCTTATTACGGGAGGGTGAGGGCGGCCTCGGCT 657
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    265 ACCAGTGAAACCTCAGACATACAGGAACCTTATTACGGGAGGGTGAGGGCGGCCTCGGCT 324

Qy    658 GGGAGCTACTCAGAATGGAGCATGACGCCGCGGTTCACTCCCTGGTGGGAAACAAAAATA 717
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    325 GGGAGCTACTCAGAATGGAGCATGACGCCGCGGTTCACTCCCTGGTGGGAAACAAAAATA 384

Qy    718 GATCCTCCAGTCATGAATATAACCCAAGTCAATGGCTCTTTGTTGGTAATTCTCCATGCT 777
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    385 GATCCTCCAGTCATGAATATAACCCAAGTCAATGGCTCTTTGTTGGTAATTCTCCATGCT 444

Qy    778 CCAAATTTACCATATAGATACCAAAAGGAAAAAAATGTATCTATAGAAGATTACTATGAA 837
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    445 CCAAATTTACCATATAGATACCAAAAGGAAAAAAATGTATCTATAGAAGATTACTATGAA 504

Qy    838 CTACTATACCGAGTTTTTATAATTAACAATTCACTAGAAAAGGAGCAAAAGGTTTATGAA 897
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    505 CTACTATACCGAGTTTTTATAATTAACAATTCACTAGAAAAGGAGCAAAAGGTTTATGAA 564

Qy    898 GGGGCTCACAGAGCGGTTGAAATTGAAGCTCTAACACCACACTCCAGCTACTGTGTAGTG 957
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    565 GGGGCTCACAGAGCGGTTGAAATTGAAGCTCTAACACCACACTCCAGCTACTGTGTAGTG 624

Qy    958 GCTGAAATATATCAGCCCATGTTAGACAGAAGAAGTCAGAGAAGTGAAGAGAGATGTGTG 1017
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    625 GCTGAAATATATCAGCCCATGTTAGACAGAAGAAGTCAGAGAAGTGAAGAGAGATGTGTG 684

Qy   1018 GAAATTCCATGA 1029
          ||||||||||||
Db    685 GAAATTCCATGA 696
```

RESULT 11
AAD06414
ID AAD06414 standard; cDNA; 696 BP.
XX
AC AAD06414;
XX

```
DT   10-AUG-2001  (first entry)
XX
DE   Human DNAX cytokine receptor subunit 4.2 (DCRS4.2) cDNA.
XX
KW   Human; immunomodulator; DNAX cytokine receptor subunit 4.2; DCRS4.2;
KW   therapy; immunological disorder; drug screening; cell development;
KW   chromosome 6q24.1-25.2; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..696
FT                   /*tag=  a
FT                   /product= "Human DNAX cytokine receptor subunit 4.2
FT                   (DCRS4.2)"
FT   sig_peptide     1..63
FT                   /*tag=  b
FT   mat_peptide     64..693
FT                   /*tag=  c
FT                   /product= "Human mature DNAX cytokine receptor
FT                   subunit 4.2 (DCRS4.2)"
XX
PN   WO200136467-A2.
XX
PD   25-MAY-2001.
XX
PF   16-NOV-2000; 2000WO-US31363.
XX
PR   18-NOV-1999;   99US-0443060.
PR   13-DEC-1999;   99US-0170320.
XX
PA   (SCHE ) SCHERING CORP.
XX
PI   Gorman DM;
XX
DR   WPI; 2001-343800/36.
DR   P-PSDB; AAE02460.
XX
PT   New mammalian receptor proteins related to cytokine receptors, useful
PT   for regulating cell development and for diagnosis and treatment of
PT   immunological disorders -
XX
PS   Claim 16; Page 22; 124pp; English.
XX
CC   The present sequence is human DNAX cytokine receptor subunit 4.2
CC   (DCRS4.2) cDNA. DCRS4 gene is located on chromosome 6q24.1-25.2.
CC   Cytokine receptors, fragments and antibodies are useful for treating
CC   immunological disorders. DCRS3 (50R), DCRS4 (cytor) or fragments are
CC   useful in drug screening to identify compounds having binding affinity
CC   to the receptor subunit. Modulators of DCRS are useful for modulating
CC   the physiology or development of a cell or tissue culture cells. A
CC   purified DCRS is useful as a reagent to detect antibodies generated in
CC   response to the presence of elevated levels of expression, or
CC   immunological disorders which lead to production of antibody to the
CC   endogenous receptor. Cytokine receptor sequences are useful as probes
CC   for detecting levels of the cytokine receptor in patients suspected of
CC   having an immunological disorder. Antibodies have therapeutic value, are
CC   useful as potent antagonist, in detecting or quantifying ligands, for
CC   isolating DCRS proteins and peptides, to screen expression libraries for
CC   particular expression products, to raise anti-idiotypic antibodies and
CC   for detecting or diagnosing various immunological conditions related to
CC   expression of the protein or cells which express the protein.
XX
SQ   Sequence 696 BP; 224 A; 141 C; 157 G; 174 T; 0 other;

  Query Match             44.6%;  Score 588.4;  DB 22;  Length 696;
  Best Local Similarity   87.8%;  Pred. No. 2.5e-112;
  Matches  695;  Conservative    0;  Mismatches    1;  Indels   96;  Gaps    1;

Qy     238 ATGATGCCTAAACATTGCTTTCTAGGCTTCCTCATCAGTTTCTTCCTTACTGGTGTAGCA 297
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 ATGATGCCTAAACATTGCTTTCTAGGCTTCCTCATCAGTTTCTTCCTTACTGGTGTAGCA 60

Qy     298 GGAACTCAGTCAACGCATGAGTCTCTGAAGCCTCAGAGGGTACAATTTCAGTCCCGAAAT 357
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 GGAACTCAGTCAACGCATGAGTCTCTGAAGCCTCAGAGGGTACAATTTCAGTCCCGAAAT 120

Qy     358 TTTCACAACATTTTGCAATGGCAGCCTGGGAGGGCACTTACTGGCAACAGCAGTGTCTAT 417
           ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db     121 TTTCACAACATTTTGCAATGGCAGCCCGGGAGGGCACTTACTGGCAACAGCAGTGTCTAT 180

Qy     418 TTTGTGCAGTACAAAATCATGTTCTCATGCAGCATGAAAAGCTCTCACCAGAAGCCAAGT 477
           |||||||||||||||||
Db     181 TTTGTGCAGTACAAAAT---------------------------------------------- 197

Qy     478 GGATGCTGGCAGCACATTTCTTGTAACTTCCCAGGCTGCAGAACATTGGCTAAATATGGA 537
                                                               |||||||
Db     198 ----------------------------------------------------ATATGGA 204

Qy     538 CAGAGACAATGGAAAAATAAAGAAGACTGTTGGGGTACTCAAGAACTCTCTTGTGACCTT 597
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     205 CAGAGACAATGGAAAAATAAAGAAGACTGTTGGGGTACTCAAGAACTCTCTTGTGACCTT 264

Qy     598 ACCAGTGAAACCTCAGACATACAGGAACCTTATTACGGGAGGGTGAGGGCGGCCTCGGCT 657
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     265 ACCAGTGAAACCTCAGACATACAGGAACCTTATTACGGGAGGGTGAGGGCGGCCTCGGCT 324

Qy     658 GGGAGCTACTCAGAATGGAGCATGACGCCGCGGTTCACTCCCTGGTGGGAAACAAAAATA 717
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     325 GGGAGCTACTCAGAATGGAGCATGACGCCGCGGTTCACTCCCTGGTGGGAAACAAAAATA 384

Qy     718 GATCCTCCAGTCATGAATATAACCCAAGTCAATGGCTCTTTGTTGGTAATTCTCCATGCT 777
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     385 GATCCTCCAGTCATGAATATAACCCAAGTCAATGGCTCTTTGTTGGTAATTCTCCATGCT 444

Qy     778 CCAAATTTACCATATAGATACCAAAAGGAAAAAAATGTATCTATAGAAGATTACTATGAA 837
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     445 CCAAATTTACCATATAGATACCAAAAGGAAAAAAATGTATCTATAGAAGATTACTATGAA 504

Qy     838 CTACTATACCGAGTTTTTATAATTAACAATTCACTAGAAAAGGAGCAAAAGGTTTATGAA 897
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     505 CTACTATACCGAGTTTTTATAATTAACAATTCACTAGAAAAGGAGCAAAAGGTTTATGAA 564

Qy     898 GGGGCTCACAGAGCGGTTGAAATTGAAGCTCTAACACCACACTCCAGCTACTGTGTAGTG 957
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     565 GGGGCTCACAGAGCGGTTGAAATTGAAGCTCTAACACCACACTCCAGCTACTGTGTAGTG 624

Qy     958 GCTGAAATATATCAGCCCATGTTAGACAGAAGAAGTCAGAGAAGTGAAGAGAGATGTGTG 1017
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     625 GCTGAAATATATCAGCCCATGTTAGACAGAAGAAGTCAGAGAAGTGAAGAGAGATGTGTG 684

Qy    1018 GAAATTCCATGA 1029
           ||||||||||||
Db     685 GAAATTCCATGA 696


RESULT 12
AAD27814
ID   AAD27814 standard; DNA; 645 BP.
XX
AC   AAD27814;
XX
DT   18-APR-2002  (first entry)
XX
DE   Human cytokine receptor gene, sbg456548CytoRa #1.
XX
KW   Human; therapy; wound healing disorder; vaccine; cancer; infection;
KW   autoimmune disorder; haematopoietic disorder; inflammation; arthritis;
KW   Parkinson's disease; Huntington's chorea; schizophrenia; antiarrhythmic;
KW   multiple sclerosis; Alzheimer's disease; analgesic; cardiant; asthma;
KW   ischaemia; stroke; AIDS; bone disease; atherosclerosis; brain disorder;
KW   depression; cardiovascular disease; myocardial infarction; renal failure;
KW   respiratory disease; liver disorder; Fanconi's syndrome; spleen disorder;
KW   type II diabetes mellitus; skeletal muscle disorder; immunosuppressive;
KW   hypersplenism; renal disease; hypoglycaemia; gastrointestinal disease;
KW   nootropic; cirrhosis; Hodgkin's disease; neuroleptic; antiinflammatory;
```

KW haemostatic; vulnerary; anticonvulsant; antirheumatic; neuroprotective;
KW nephrotropic; hypotensive; vasotropic; cytostatic; cerebroprotective;
KW allergy; cytokine receptor; gene; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..645
FT /*tag= a
FT /product= "Human cytokine receptor"
XX
PN WO200198342-A1.
XX
PD 27-DEC-2001.
XX
PF 22-JUN-2001; 2001WO-US19929.
XX
PR 22-JUN-2000; 2000US-213156P.
PR 22-JUN-2000; 2000US-213161P.
XX
(SMIK) SMITHKLINE BEECHAM CORP.
(SMIK) SMITHKLINE BEECHAM PLC.
PA (GLAX) GLAXO GROUP LTD.
XX
PI Agarwal P, Cogswell JP, Kabnic KS, Lai Y, Martensen SA;
PI Murdock PR, Smith RF, Strum JC, Xiang Z, Xie Q, Rizni SK;
XX
DR WPI; 2002-139783/18.
DR P-PSDB; AAE17319.
XX
PT Novel secreted and membrane-associated polypeptides and polynucleotides
PT useful for preventing, ameliorating or correcting dysfunction or
PT disease including diabetes, cancer, hypertension and growth
PT abnormalities -
XX
PS Claim 2; Page 97; 138pp; English.
XX
CC The invention relates to secreted and membrane-associated polypeptides
CC and polynucleotides. The sequences of the invention are useful in
CC diagnostic assays for detecting diseases associated with inappropriate
CC activity or levels of these polynucleotides, and in identifying their
CC agonists and antagonists that are potentially useful in therapy. The
CC sequences of the invention are useful as vaccines for inducing
CC immunological response. The sequences of the invention are useful for
CC treating cancers, infections, autoimmune disorders, haematopoietic
CC disorders, wound healing disorders, cholesteryl ester storage disease,
CC inflammation, congenital muscular dystrophy, junctional epidermolysis
CC bullosa, Parkinson's disease, Huntington's chorea, multiple sclerosis,
CC viral and bacterial infections, Alzheimer's disease, asthma, arthritis,
CC allergies, schizophrenia, sbg442445PROa-associated disorders,
CC septicaemia, psoriasis, inflammatory bowel disease, transplant rejection,
CC graft verse host disease, ischaemia, stroke, acute respiratory disease
CC syndrome, restenosis, brain injury, AIDS, bone diseases, atherosclerosis,
CC brain disorders including parasupranuclear palsy, myotonic dystrophy,
CC depression, anxiety disorders and sleep disorders, cardiovascular
CC diseases including congestive heart failure and myocardial infarction,
CC respiratory diseases including chronic obstructive pulmonary disease,
CC acute bronchitis and adult respiratory distress syndrome, liver disorders
CC including hypercholesterolaemia, hypertriglyceridaemia, cirrhosis, viral
CC and non-viral hepatitis, type II diabetes mellitus, renal disease
CC including acute and chronic renal failure, glomerulonephritis, Fanconi's
CC syndrome, cystinuria, skeletal muscle disorders including hypoglycaemia
CC and tendinitis, gastrointestinal diseases including intestinal
CC obstruction and tropical sprue, spleen disorders including hypersplenism,
CC Hodgkin's disease and malignant lymphoma, testicular cancer, male
CC reproductive diseases including low testosterone and male infertility.
CC The present sequence is human cytokine receptor gene.
XX
SQ Sequence 645 BP; 215 A; 127 C; 150 G; 153 T; 0 other;

Query Match 40.4%; Score 533; DB 24; Length 645;
Best Local Similarity 86.9%; Pred. No. 6.8e-101;
Matches 639; Conservative 0; Mismatches 0; Indels 96; Gaps 1;

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Qy    295 GCAGGAACTCAGTCAACGCATGAGTCTCTGAAGCCTCAGAGGGTACAATTTCAGTCCCGA 354
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      7 GCAGGAACTCAGTCAACGCATGAGTCTCTGAAGCCTCAGAGGGTACAATTTCAGTCCCGA 66

Qy    355 AATTTTCACAACATTTTGCAATGGCAGCCTGGGAGGGCACTTACTGGCAACAGCAGTGTC 414
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     67 AATTTTCACAACATTTTGCAATGGCAGCCTGGGAGGGCACTTACTGGCAACAGCAGTGTC 126

Qy    415 TATTTTGTGCAGTACAAAATCATGTTCTCATGCAGCATGAAAAGCTCTCACCAGAAGCCA 474
          ||||||||||||||||||||
Db    127 TATTTTGTGCAGTACAAAAT---------------------------------------- 146

Qy    475 AGTGGATGCTGGCAGCACATTTCTTGTAACTTCCCAGGCTGCAGAACATTGGCTAAATAT 534
                                                                ||||
Db    147 ----------------------------------------------------------ATAT 150

Qy    535 GGACAGAGACAATGGAAAAATAAAGAAGACTGTTGGGGTACTCAAGAACTCTCTTGTGAC 594
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    151 GGACAGAGACAATGGAAAAATAAAGAAGACTGTTGGGGTACTCAAGAACTCTCTTGTGAC 210

Qy    595 CTTACCAGTGAAACCTCAGACATACAGGAACCTTATTACGGGAGGGTGAGGGCGGCCTCG 654
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    211 CTTACCAGTGAAACCTCAGACATACAGGAACCTTATTACGGGAGGGTGAGGGCGGCCTCG 270

Qy    655 GCTGGGAGCTACTCAGAATGGAGCATGACGCCGCGGTTCACTCCCTGGTGGGAAACAAAA 714
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    271 GCTGGGAGCTACTCAGAATGGAGCATGACGCCGCGGTTCACTCCCTGGTGGGAAACAAAA 330

Qy    715 ATAGATCCTCCAGTCATGAATATAACCCAAGTCAATGGCTCTTTGTTGGTAATTCTCCAT 774
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    331 ATAGATCCTCCAGTCATGAATATAACCCAAGTCAATGGCTCTTTGTTGGTAATTCTCCAT 390

Qy    775 GCTCCAAATTTACCATATAGATACCAAAAGGAAAAAAATGTATCTATAGAAGATTACTAT 834
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    391 GCTCCAAATTTACCATATAGATACCAAAAGGAAAAAAATGTATCTATAGAAGATTACTAT 450

Qy    835 GAACTACTATACCGAGTTTTTATAATTAACAATTCACTAGAAAAGGAGCAAAAGGTTTAT 894
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    451 GAACTACTATACCGAGTTTTTATAATTAACAATTCACTAGAAAAGGAGCAAAAGGTTTAT 510

Qy    895 GAAGGGGCTCACAGAGCGGTTGAAATTGAAGCTCTAACACCACACTCCAGCTACTGTGTA 954
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    511 GAAGGGGCTCACAGAGCGGTTGAAATTGAAGCTCTAACACCACACTCCAGCTACTGTGTA 570

Qy    955 GTGGCTGAAATATATCAGCCCATGTTAGACAGAAGAAGTCAGAGAAGTGAAGAGAGATGT 1014
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    571 GTGGCTGAAATATATCAGCCCATGTTAGACAGAAGAAGTCAGAGAAGTGAAGAGAGATGT 630

Qy   1015 GTGGAAATTCCATGA 1029
          |||||||||||||||
Db    631 GTGGAAATTCCATGA 645
```

RESULT 13
AAD06410
ID AAD06410 standard; cDNA; 750 BP.
XX
AC AAD06410;
XX
DT 10-AUG-2001 (first entry)
XX
DE Human DNAX cytokine receptor subunit 4.1 (DCRS4.1) cDNA.
XX
KW Human; immunomodulator; DNAX cytokine receptor subunit 4.1; DCRS4.1;
KW therapy; immunological disorder; drug screening; cell development;
KW chromosome 6q24.1-25.2; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..750
FT /*tag= a

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FT                   /product= "Human DNAX cytokine receptor subunit 4.1
FT                   (DCRS4.1)"
FT   sig_peptide     1..63
FT                   /*tag=  b
FT   mat_peptide     64..747
FT                   /*tag=  c
FT                   /product= "Human mature DNAX cytokine receptor
FT                   subunit 4.1 (DCRS4.1)"
XX
PN   WO200136467-A2.
XX
PD   25-MAY-2001.
XX
PF   16-NOV-2000; 2000WO-US31363.
XX
PR   18-NOV-1999;   99US-0443060.
PR   13-DEC-1999;   99US-0170320.
XX
PA   (SCHE ) SCHERING CORP.
XX
PA   Gorman DM;
XX
DR   WPI; 2001-343800/36.
DR   P-PSDB; AAE02458.
XX
PT   New mammalian receptor proteins related to cytokine receptors, useful
PT   for regulating cell development and for diagnosis and treatment of
PT   immunological disorders -
XX
PS   Claim 16; Page 21-22; 124pp; English.
XX
CC   The present sequence is human DNAX cytokine receptor subunit 4.1
CC   (DCRS4.1) cDNA. DCRS4 gene is located on chromosome 6q24.1-25.2.
CC   Cytokine receptors, fragments and antibodies are useful for treating
CC   immunological disorders. DCRS3 (50R), DCRS4 (cytor) or fragments are
CC   useful in drug screening to identify compounds having binding affinity
CC   to the receptor subunit. Modulators of DCRS are useful for modulating
CC   the physiology or development of a cell or tissue culture cells. A
CC   purified DCRS is useful as a reagent to detect antibodies generated in
CC   response to the presence of elevated levels of expression, or
CC   immunological disorders which lead to production of antibody to the
CC   endogenous receptor. Cytokine receptor sequences are useful as probes
CC   for detecting levels of the cytokine receptor in patients suspected of
CC   having an immunological disorder. Antibodies have therapeutic value, are
CC   useful as potent antagonist, in detecting or quantifying ligands, for
CC   isolating DCRS proteins and peptides, to screen expression libraries for
CC   particular expression products, to raise anti-idiotypic antibodies and
CC   for detecting or diagnosing various immunological conditions related to
CC   expression of the protein or cells which express the protein.

SQ   Sequence 750 BP; 259 A; 147 C; 164 G; 180 T; 0 other;
```

Query Match 34.1%; Score 449.2; DB 22; Length 750;
Best Local Similarity 76.6%; Pred. No. 1.4e-83;
Matches 607; Conservative 0; Mismatches 143; Indels 42; Gaps 3;

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Qy    238 ATGATGCCTAAACATTGCTTTCTAGGCTTCCTCATCAGTTTCTTCCTTACTGGTGTAGCA 297
Db      1 ATGATGCCTAAACATTGCTTTCTAGGCTTCCTCATCAGTTTCTTCCTTACTGGTGTAGCA 60

Qy    298 GGAACTCAGTCAACGCATGAGTCTCTGAAGCCTCAGAGGGTACAATTTCAGTCCCGAAAT 357
Db     61 GGAACTCAGTCAACGCATGAGTCTCTGAAGCCTCAGAGGGTACAATTTCAGTCCCGAAAT 120

Qy    358 TTTCACAACATTTTGCAATGGCAGCCTGGGAGGGCACTTACTGGCAACAGCAGTGTCTAT 417
Db    121 TTTCACAACATTTTGCAATGGCAGCCTGGGAGGGCACTTACTGGCAACAGCAGTGTCTAT 180

Qy    418 TTTGTGCAGTACAAAATCATGTTCTCATGCAGCATGAAAAGCTCTCACCAGAAGCCAAGT 477
Db    181 TTTGTGCAGTACAAAAT-ATATGGACAGAGACAATGGAAAAATAAAGAAGACTGTTGGGG 239

Qy    478 GGATGCTGGCAGCACATTTCTTGTAACTTCCCAGGCTGCAGAACATTGGCTAAATATGGA 537
Db    240 TACTCAAGAACTCTCTTGTGACCTTACCAGTGAAACCTCAGACATACAGGAACCTTATTA 299

Qy    538 CAGAGACAATGGAAAAATAAAGAAGACTGTTGGGGTACTCAAGAACTCTCTTGTGACCTT 597
Db    300 CGGGAGGAGGGGCAAAAATAAAAATAAAG-----------GGAATCCTTGGGGGCCAAA 347

Qy    598 ACCAGTGAAACCTCAGACATACAGGAACCTTATTACGGGAGGGTGAGGGCGGCCTCGGCT 657
Db    348 ACAAAGTAAACGGAAATCAAAGGGGAACCAGA--------------------------- 379

Qy    658 GGGAGCTACTCAGAATGGAGCATGACGCCGCGGTTCACTCCCTGGTGGGAAACAAAAATA 717
Db    380 -AGACCAACACAGTGACTGCCCCAGCTGCCCTGAAGGCATTTGCTGGATGTGCAAAAATA 438

Qy    718 GATCCTCCAGTCATGAATATAACCCAAGTCAATGGCTCTTTGTTGGTAATTCTCCATGCT 777
Db    439 GATCCTCCAGTCATGAATATAACCCAAGTCAATGGCTCTTTGTTGGTAATTCTCCATGCT 498

Qy    778 CCAAATTTACCATATAGATACCAAAAGGAAAAAAATGTATCTATAGAAGATTACTATGAA 837
Db    499 CCAAATTTACCATATAGATACCAAAAGGAAAAAAATGTATCTATAGAAGATTACTATGAA 558

Qy    838 CTACTATACCGAGTTTTTATAATTAACAATTCACTAGAAAAGGAGCAAAAGGTTTATGAA 897
Db    559 CTACTATACCGAGTTTTTATAATTAACAATTCACTAGAAAAGGAGCAAAAGGTTTATGAA 618

Qy    898 GGGGCTCACAGAGCGGTTGAAATTGAAGCTCTAACACCACACTCCAGCTACTGTGTAGTG 957
Db    619 GGGGCTCACAGAGCGGTTGAAATTGAAGCTCTAACACCACACTCCAGCTACTGTGTAGTG 678

Qy    958 GCTGAAATATATCAGCCCATGTTAGACAGAAGAAGTCAGAGAAGTGAAGAGAGATGTGTG 1017
Db    679 GCTGAAATATATCAGCCCATGTTAGACAGAAGAAGTCAGAGAAGTGAAGAGAGATGTGTG 738

Qy   1018 GAAATTCCATGA 1029
Db    739 GAAATTCCATGA 750
```

```
RESULT 14
AAL45999
ID   AAL45999 standard; cDNA; 750 BP.
XX
AC   AAL45999;
XX
DT   08-AUG-2002  (first entry)
XX
DE   Human cytokine receptor variant 1 coding sequence.
XX
KW   Human; cytokine receptor; immune disease; psoriasis; cancer; infection;
KW   rheumatoid arthritis; multiple sclerosis; Crohn's disease;
KW   ulcerative colitis; transplant rejection; abortion; antipsoriatic;
KW   immunosuppressive; antirheumatic; antiarthritic; neuroprotective;
KW   antiinflammatory; antiulcer; cytostatic; dermatological;
KW   chromosome 6q24.1-25.2; receptor; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..750
FT                   /*tag=  a
FT                   /product= "cytokine receptor variant 1"
XX
PN   EP1191035-A2.
XX
PD   27-MAR-2002.
XX
PF   24-AUG-2001; 2001EP-0250307.
XX
PR   25-SEP-2000; 2000DE-1048626.
PR   17-NOV-2000; 2000DE-1058907.
PR   19-DEC-2000; 2000DE-1064906.
```

XX
PA (SCHD) SCHERING AG.
XX
PI Weiss B, Sabat R, Assadullah K, Toshi L;
XX
DR WPI; 2002-332210/37.
DR P-PSDB; AAO17380.
XX
PT New nucleic acid encoding soluble cytokine receptor, useful for
PT diagnosis and treatment of e.g. immune disease, also related protein
PT and antibodies -
XX
PS Claim 1; Page 12; 21pp; German.
XX
CC The present invention provides the protein and coding sequences of 3
CC variants of a human cytokine receptor. The sequences can be used in the
CC diagnosis, prevention and treatment of immune diseases, including
CC psoriasis, cancer, chronic/life-threatening infections, rheumatoid
CC arthritis, multiple sclerosis, Crohn's disease, ulcerative colitis and
CC transplant rejection and in reproductive medicine, e.g. for diagnosing
CC abnormal immune reactions which cause abortions. The present sequence is
CC the coding sequence of variant 1 of the invention.
XX
SQ Sequence 750 BP; 259 A; 147 C; 164 G; 180 T; 0 other;

Query Match 34.1%; Score 449.2; DB 24; Length 750;
Best Local Similarity 76.6%; Pred. No. 1.4e-83;
Matches 607; Conservative 0; Mismatches 143; Indels 42; Gaps 3;

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Qy    238 ATGATGCCTAAACATTGCTTTCTAGGCTTCCTCATCAGTTTCTTCCTTACTGGTGTAGCA 297
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGATGCCTAAACATTGCTTTCTAGGCTTCCTCATCAGTTTCTTCCTTACTGGTGTAGCA 60

Qy    298 GGAACTCAGTCAACGCATGAGTCTCTGAAGCCTCAGAGGGTACAATTTCAGTCCCGAAAT 357
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Db     61 GGAACTCAGTCAACGCATGAGTCTCTGAAGCCTCAGAGGGTACAATTTCAGTCCCGAAAT 120

Qy    358 TTTCACAACATTTTGCAATGGCAGCCTGGGAGGGCACTTACTGGCAACAGCAGTGTCTAT 417
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 TTTCACAACATTTTGCAATGGCAGCCTGGGAGGGCACTTACTGGCAACAGCAGTGTCTAT 180

Qy    418 TTTGTGCAGTACAAAATCATGTTCTCATGCAGCATGAAAAGCTCTCACCAGAAGCCAAGT 477
          |||||||||||||||| || |   ||   |  ||| |||  |          |    |
Db    181 TTTGTGCAGTACAAAAT-ATATGGACAGAGACAATGGAAAAATAAAGAAGACTGTTGGGG 239

Qy    478 GGATGCTGGCAGCACATTTCTTGTAACTTCCCAGGCTGCAGAACATTGGCTAAATATGGA 537
          |   |    | | | |    | ||     |  |  ||||      |  |  |    |
Db    240 TACTCAAGAACTCTCTTGTGACCTTACCAGTGAAACCTCAGACATACAGGAACCTTATTA 299

Qy    538 CAGAGACAATGGAAAAATAAAGAAGACTGTTGGGGTACTCAAGAACTCTCTTGTGACCTT 597
          | |    |  || ||||  || || |  |           |||  ||   | | |
Db    300 CGGGAGGAGGGGCAAAAATAAAAATAAAG-----------GGAATCCTTGGGGGCCAAA 347

Qy    598 ACCAGTGAAACCTCAGACATACAGGAACCTTATTACGGGAGGGTGAGGGCGGCCTCGGCT 657
          || |   ||||   |  || |  ||||||  |
Db    348 ACAAAGTAAACGGAAATCAAAGGGGAACCAGA-------------------------- 379

Qy    658 GGGAGCTACTCAGAATGGAGCATGACGCCGCGGTTCACTCCCTGGTGGGAAACAAAAATA 717
            || | || |||       |    | | | |    |      |    ||||||||
Db    380 -AGACCAACACAGTGACTGCCCCAGCTGCCCTGAAGGCATTTGCTGGATGTGCAAAAATA 438

Qy    718 GATCCTCCAGTCATGAATATAACCCAAGTCAATGGCTCTTTGTTGGTAATTCTCCATGCT 777
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    439 GATCCTCCAGTCATGAATATAACCCAAGTCAATGGCTCTTTGTTGGTAATTCTCCATGCT 498

Qy    778 CCAAATTTACCATATAGATACCAAAAGGAAAAAAATGTATCTATAGAAGATTACTATGAA 837
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    499 CCAAATTTACCATATAGATACCAAAAGGAAAAAAATGTATCTATAGAAGATTACTATGAA 558

Qy    838 CTACTATACCGAGTTTTTATAATTAACAATTCACTAGAAAAGGAGCAAAAGGTTTATGAA 897
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    559 CTACTATACCGAGTTTTTATAATTAACAATTCACTAGAAAAGGAGCAAAAGGTTTATGAA 618
```

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Qy    898 GGGGCTCACAGAGCGGTTGAAATTGAAGCTCTAACACCACACTCCAGCTACTGTGTAGTG 957
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Qy    958 GCTGAAATATATCAGCCCATGTTAGACAGAAGAAGTCAGAGAAGTGAAGAGAGATGTGTG 1017
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    679 GCTGAAATATATCAGCCCATGTTAGACAGAAGAAGTCAGAGAAGTGAAGAGAGATGTGTG 738

Qy   1018 GAAATTCCATGA 1029
          ||||||||||||
Db    739 GAAATTCCATGA 750
```

RESULT 15
AAD06415
ID AAD06415 standard; DNA; 693 BP.
XX
AC AAD06415;
XX
DT 10-AUG-2001 (first entry)
XX
DE Human DNAX cytokine receptor subunit 4.2 reverse translational DNA.
XX
KW Human; immunomodulator; DNAX cytokine receptor subunit 4.2; DCRS4.2;
KW therapy; immunological disorder; drug screening; cell development;
KW chromosome 6q24.1-25.2; ds.
XX
OS Homo sapiens.
XX
PN WO200136467-A2.
XX
PD 25-MAY-2001.
XX
PF 16-NOV-2000; 2000WO-US31363.
XX
PR 18-NOV-1999; 99US-0443060.
PR 13-DEC-1999; 99US-0170320.
XX
PA (SCHE) SCHERING CORP.
XX
PI Gorman DM;
XX
DR WPI; 2001-343800/36.
XX
PT New mammalian receptor proteins related to cytokine receptors, useful
PT for regulating cell development and for diagnosis and treatment of
PT immunological disorders -
XX
PS Disclosure; Page 25; 124pp; English.
XX
CC The present sequence is human DNAX cytokine receptor subunit 4.2
CC (DCRS4.2) reverse translational DNA. DCRS4 gene is located on
CC chromosome 6q24.1-25.2. Cytokine receptors, fragments and antibodies are
CC useful for treating immunological disorders. DCRS3 (50R), DCRS4 (cytor)
CC or fragments are useful in drug screening to identify compounds having
CC binding affinity to the receptor subunit. Modulators of DCRS are useful
CC for modulating the physiology or development of a cell or tissue culture
CC cells. A purified DCRS is useful as a reagent to detect antibodies
CC generated in response to the presence of elevated levels of expression,
CC or immunological disorders which lead to production of antibody to the
CC endogenous receptor. Cytokine receptor sequences are useful as probes
CC for detecting levels of the cytokine receptor in patients suspected of
CC having an immunological disorder. Antibodies have therapeutic value, are
CC useful as potent antagonist, in detecting or quantifying ligands, for
CC isolating DCRS proteins and peptides, to screen expression libraries for
CC particular expression products, to raise anti-idiotypic antibodies and
CC for detecting or diagnosing various immunological conditions related to
CC expression of the protein or cells which express the protein.
XX
SQ Sequence 693 BP; 131 A; 70 C; 108 G; 93 T; 291 other;

Query Match 30.2%; Score 398.2; DB 22; Length 693;
Best Local Similarity 51.0%; Pred. No. 4.9e-73;

Matches 402; Conservative 179; Mismatches 111; Indels 96; Gaps 1;

```
Qy    238 ATGATGCCTAAACATTGCTTTCTAGGCTTCCTCATCAGTTTCTTCCTTACTGGTGTAGCA 297
          ||||||||  ||:||:||:||::|  ||  ||::|  ||:::  ||:||::|  ||  ||  ||  ||
Db      1 ATGATGCCNAARCAYTGYTTYYTNGGNTTYYTNATHWSNTTYTTYYTNACNGGNGTNGCN 60

Qy    298 GGAACTCAGTCAACGCATGAGTCTCTGAAGCCTCAGAGGGTACAATTTCAGTCCCGAAAT 357
          ||  ||  ||:::  ||  ||:||:::  :|  ||:||  ||::|  ||  ||:||:||:::  :|  ||:
Db     61 GGNACNCARWSNACNCAYGARWSNYTNAARCCNCARMGNGTNCARTTYCARWSNMGNAAY 120

Qy    358 TTTCACAACATTTTGCAATGGCAGCCTGGGAGGGCACTTACTGGCAACAGCAGTGTCTAT 417
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Db    121 TTYCAYAAYATHYTNCARTGGCARCCNGGNMGNGCNYTNACNGGNAAYWSNWSNGTNTAY 180

Qy    418 TTTGTGCAGTACAAAATCATGTTCTCATGCAGCATGAAAAGCTCTCACCAGAAGCCAAGT 477
          ||:||  ||:||:||:||
Db    181 TTYGTNCARTAYAARAT----------------------------------------- 197

Qy    478 GGATGCTGGCAGCACATTTCTTGTAACTTCCCAGGCTGCAGAACATTGGCTAAATATGGA 537
                                                                :||:||
Db    198 ----------------------------------------------------HTAYGGN 204

Qy    538 CAGAGACAATGGAAAAATAAAGAAGACTGTTGGGGTACTCAAGAACTCTCTTGTGACCTT 597
          ||::|  ||:|||||:||:||:||:||:||:|||||  ||  ||:||::|  ::  ||:||::|
Db    205 CARMGNCARTGGAARAAYAARGARGAYTGYTGGGGNACNCARGARYTNWSNTGYGAYYTN 264

Qy    598 ACCAGTGAAACCTCAGACATACAGGAACCTTATTACGGGAGGGTGAGGGCGGCCTCGGCT 657
          ||  ::  ||:||  ::  ||:||:||:||:||  ||:||:||  :|  ||  :|  ||  ||  ::  ||
Db    265 ACNWSNGARACNWSNGAYATHCARGARCCNTAYTAYGGNMGNGTNMGNGCNGCNWSNGCN 324

Qy    658 GGGAGCTACTCAGAATGGAGCATGACGCCGCGGTTCACTCCCTGGTGGGAAACAAAAATA 717
          ||  ::  ||:::  ||:|||::  |||||  ||  :|  ||:||  ||  ||||||||:||  ||:||:
Db    325 GGNWSNTAYWSNGARTGGWSNATGACNCCNMGNTTYACNCCNTGGTGGGARACNAARATH 384

Qy    718 GATCCTCCAGTCATGAATATAACCCAAGTCAATGGCTCTTTGTTGGTAATTCTCCATGCT 777
          ||:||  ||  ||  |||||:||:||  ||:||  ||:||  ::  :|  :|  ||  ||::|  ||:||
Db    385 GAYCCNCCNGTNATGAAYATHACNCARGTNAAYGGNWSNYTNYTNGTNATHYTNCAYGCN 444

Qy    778 CCAAATTTACCATATAGATACCAAAAGGAAAAAAATGTATCTATAGAAGATTACTATGAA 837
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Db    445 CCNAAYYTNCCNTAYMGNTAYCARAARGARAARAAYGTNWSNATHGARGAYTAYTAYGAR 504

Qy    838 CTACTATACCGAGTTTTTATAATTAACAATTCACTAGAAAAGGAGCAAAAGGTTTATGAA 897
          :|  :|  ||::|  ||  ||:||:||:||:||:::  :|  ||:||:||:||:||:||  ||:||:
Db    505 YTNYTNTAYMGNGTNTTYATHATHAAYAAYWSNYTNGARAARGARCARAARGTNTAYGAR 564

Qy    898 GGGGCTCACAGAGCGGTTGAAATTGAAGCTCTAACACCACACTCCAGCTACTGTGTAGTG 957
          ||  ||  ||::|  ||  ||  ||:||:||:||  :|  ||  ||  ||:::  ::  ||:||:||  ||
Db    565 GGNGCNCAYMGNGCNGTNGARATHGARGCNYTNACNCCNCAYWSNWSNTAYTGYGTNGTN 624

Qy    958 GCTGAAATATATCAGCCCATGTTAGACAGAAGAAGTCAGAGAAGTGAAGAGAGATGTGTG 1017
          ||  ||:||:||:||:||  |||:|  ||::|  :|  ::  ||::|  ::  ||:||::|  ||:||
Db    625 GCNGARATHTAYCARCCNATGYTNGAYMGNMGNWSNCARMGNWSNGARGARMGNTGYGTN 684

Qy   1018 GAAATTCC 1025
          ||:||:||
Db    685 GARATHCC 692
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Search completed: December 22, 2002, 07:51:30
Job time : 265 secs

GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: December 22, 2002, 07:43:01 ; Search time 1969 Seconds
(without alignments)
10840.859 Million cell updates/sec

Title: US-09-964-994-1
Perfect score: 1318
Sequence: 1 cagtttcttcatctgtaaca.....aaaaaaaaaaaaaaaaaaaa 1318

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
	1	686	52.0	698	10	AV714177	AV714177 AV714177
	2	284.4	21.6	632	10	BB636466	BB636466 BB636466
	3	222.4	16.9	663	10	BB222214	BB222214 BB222214
	4	160	12.1	572	10	BB637530	BB637530 BB637530
	5	124.2	9.4	494	12	BE809214	BE809214 214604 MA
c	6	106.2	8.1	548	17	BH117626	BH117626 RPCI-24-2
c	7	84.6	6.4	645	17	AZ722045	AZ722045 RPCI-24-1
c	8	81	6.1	583	10	AW833620	AW833620 QV4-TT000
c	9	77.4	5.9	311	9	AL513907	AL513907 AL513907
	10	77	5.8	311	9	AL513907	AL513907 AL513907
c	11	76.2	5.8	454	9	AL513951	AL513951 AL513951
c	12	75.8	5.8	304	9	AL514919	AL514919 AL514919
c	13	75.4	5.7	319	9	AL513977	AL513977 AL513977
c	14	75.2	5.7	365	9	AL515373	AL515373 AL515373
c	15	74.4	5.6	503	9	AL513809	AL513809 AL513809
c	16	74.2	5.6	366	9	AL514543	AL514543 AL514543
c	17	74.2	5.6	794	17	AZ530415	AZ530415 ENTBX01TR
	18	74	5.6	240	9	AU074171	AU074171 AU074171
c	19	73.8	5.6	353	9	AL515235	AL515235 AL515235
	20	73.8	5.6	621	10	BB666101	BB666101 BB666101
	21	73.6	5.6	458	9	AL514085	AL514085 AL514085
c	22	73.4	5.6	329	9	AL513719	AL513719 AL513719
c	23	73.4	5.6	329	9	AL514627	AL514627 AL514627
c	24	73	5.5	401	9	AL515191	AL515191 AL515191
	25	73	5.5	404	9	AL514087	AL514087 AL514087
c	26	73	5.5	638	9	AL513901	AL513901 AL513901
c	27	72.6	5.5	965	17	AZ529824	AZ529824 ENTCX56TF
c	28	72.4	5.5	449	9	AL513999	AL513999 AL513999
c	29	72	5.5	404	9	AL514087	AL514087 AL514087
	30	71.8	5.4	335	9	AL513597	AL513597 AL513597
c	31	71.8	5.4	601	9	AL513631	AL513631 AL513631
c	32	71.6	5.4	316	13	BM651303	BM651303 170006873
c	33	71.6	5.4	379	9	AL514359	AL514359 AL514359
c	34	71.6	5.4	535	14	BQ400871	BQ400871 NISC_mp11
	35	71.4	5.4	329	9	AL514627	AL514627 AL514627
	36	71.4	5.4	523	9	AL514015	AL514015 AL514015
c	37	71.2	5.4	425	9	AL514791	AL514791 AL514791
	38	71	5.4	276	14	BQ527333	BQ527333 NISC_no21
c	39	71	5.4	276	14	BQ527333	BQ527333 NISC_no21
c	40	71	5.4	309	9	AL514691	AL514691 AL514691
	41	71	5.4	313	14	BQ391420	BQ391420 NISC_mq18
c	42	71	5.4	313	14	BQ391420	BQ391420 NISC_mq18
	43	71	5.4	367	14	BQ525045	BQ525045 NISC_no08
c	44	71	5.4	477	14	BQ390789	BQ390789 NISC_mq15
c	45	71	5.4	501	14	BQ525537	BQ525537 NISC_no11

ALIGNMENTS

RESULT 1
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LOCUS AV714177 698 bp mRNA linear EST 11-OCT-2000
DEFINITION AV714177 DCB Homo sapiens cDNA clone DCBAWF09 5', mRNA sequence.
ACCESSION AV714177
VERSION AV714177.1 GI:10795694
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 698)
AUTHORS Xu,X., Gu,J., Liu,F., Qu,J., Zhao,M., Li,Y., Huang,Q., Zhou,J., Song,H., Gu,Y., Yang,Y., Gao,G., Xiao,H., Li,N., Qian,B., Gao,X., Cheng,Z., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu ,G., Cheng,Z. and Han,Z.
TITLE Homo sapiens cDNA DCB clones
JOURNAL Unpublished (2000)
COMMENT Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
FEATURES Location/Qualifiers
source 1. .698
/organism="Homo sapiens"

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                     /clone="DCBAWF09"
                     /clone_lib="DCB"
                     /cell_type="dendritic cells"
                     /dev_stage="mature"
                     /lab_host="BM25.8"
                     /note="Vector: pTriplEx2; Site_1: sfiIA; Site_2: sfiIB"
BASE COUNT      219 a    131 c    146 g    201 t      1 others
ORIGIN

  Query Match             52.0%;  Score 686;  DB 10;  Length 698;
  Best Local Similarity   99.1%;  Pred. No. 2.2e-93;
  Matches  689;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy     547 TGGAAAAATAAAGAAGACTGTTGGGGTACTCAAGAACTCTCTTGTGACCTTACCAGTGAA 606
           ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db       1 TGGAAAAATAAAGAAGACTGGGGGGGTACTCAAGAACTCTCTTGTGACCTTACCAGTGAA 60

Qy     607 ACCTCAGACATACAGGAACCTTATTACGGGAGGGTGAGGGCGGCCTCGGCTGGGAGCTAC 666
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 ACCTCAGACATACAGGAACCTTATTACGGGAGGGTGAGGGCGGCCTCGGCTGGGAGCTAC 120

Qy     667 TCAGAATGGAGCATGACGCCGCGGTTCACTCCCTGGTGGGAAACAAAAATAGATCCTCCA 726
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 TCAGAATGGAGCATGACGCCGCGGTTCACTCCCTGGTGGGAAACAAAAATAGATCCTCCA 180

Qy     727 GTCATGAATATAACCCAAGTCAATGGCTCTTTGTTGGTAATTCTCCATGCTCCAAATTTA 786
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 GTCATGAATATAACCCAAGTCAATGGCTCTTTGTTGGTAATTCTCCATGCTCCAAATTTA 240

Qy     787 CCATATAGATACCAAAAGGAAAAAAATGTATCTATAGAAGATTACTATGAACTACTATAC 846
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Db     241 CCATATAGATACCAAAAGGAAAAAAATGTATCTATAGAAGATTACTATGAACTACTATAC 300

Qy     847 CGAGTTTTTATAATTAACAATTCACTAGAAAAGGAGCAAAAGGTTTATGAAGGGGCTCAC 906
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Db     301 CGAGTTTTTATAATTAACAATTCACTAGAAAAGGAGCAAAAGGTTTATGAAGGGGCTCAC 360

Qy     907 AGAGCGGTTGAAATTGAAGCTCTAACACCACACTCCAGCTACTGTGTAGTGGCTGAAATA 966
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Db     361 AGAGCGGTTGAAATTGAAGCTCTAACACCACACTCCAGCTACTGTGTAGTGGCTGAAATA 420

Qy     967 TATCAGCCCATGTTAGACAGAAGAAGTCAGAGAAGTGAAGAGAGATGTGTGGAAATTCCA 1026
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Qy    1027 TGACTTGTGGAATTTGGCATTCAGCAATGTGGAAATTCTAAAGCTCCCTGAGAACAGGAT 1086
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Db     481 TGACTTGTGGAATTTGGCATTCAGCAATGTGGAAATTCTAAAGCTCCCTGAGAACAGGAT 540

Qy    1087 GACTCGTGTTTGAAGGATCTTATTTAAAATTGTTTTTGTATTTTCTTAAAGCAATATTCA 1146
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 GACTCGTGTTTGAAGGATCTTATTTAAAATTGTTTTTGTATTTTCTTAAAGCAATATTCA 600

Qy    1147 CTGTTACACCTTGGGGACTTCTTTGTTTATCCATTCTTTTATCCTTTATATTTCATTTGT 1206
           ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db     601 CTGTTACACCTTGGGGACTTCTTTGNTTATCCATTCTTTTATCCTTTATATTTCATTTGT 660

Qy    1207 AAACTATATTTGAACGACATTCCCCCCGAAAAATT 1241
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Db     661 AAACTATATTTGAACGACATTCCCCCCGACTTATT 695


RESULT 2
BB636466
LOCUS       BB636466                 632 bp    mRNA    linear   EST 26-OCT-2001
DEFINITION  BB636466 RIKEN full-length enriched, adult male aorta and vein Mus
            musculus cDNA clone A530002E19 5', mRNA sequence.
ACCESSION   BB636466
VERSION     BB636466.1  GI:16472332
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 632)
  AUTHORS   Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.
            , Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda
            ,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,
            Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki
            ,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
            Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,
            Muramatsu,M. and Hayashizaki,Y.
  TITLE     RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/
            Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
            ,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
             Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new
            genes. Genome Res. . 10 (10), 1617-1630 (2000)
             wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
            Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
            ,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
            Hayashizaki,Y.
             RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer. Genome Res. .
            10 (11), 1757-1771 (2000)
             Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
            ,Y. and Hayashizaki,Y.
             Computer-based methods for the mouse full-length cDNA
            encyclopedia: real-time sequence clustering for construction of a
            nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)
             Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa
            ,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
            Hayashizaki,Y.
             Computational Analysis of Full-Length Mouse cDNAs Compared with
            Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
             Please visit our web site (http://genome.gsc.riken.go.jp) for
            further details.
             e mouse tissues.
FEATURES             Location/Qualifiers
     source          1. .632
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="A530002E19"
                     /clone_lib="RIKEN full-length enriched, adult male aorta
                     and vein"
                     /sex="male"
                     /tissue_type="aorta and vein"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /note="Site_1: SalI; Site_2: BamHI; cDNA library was
                     prepared and sequenced in Mouse Genome Encyclopedia
                     Project of Genome Exploration Research Group in Riken
                     Genomic Sciences Center and Genome Science Laboratory in
                     RIKEN. Division of Experimental Animal Research in Riken
                     contributed to prepare mouse tissues. 1st strand cDNA was
                     primed with a primer [5'
                     GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTTVN 3'], cDNA was
                     prepared by using trehalose thermo-activated reverse
                     transcriptase and subsequently enriched for full-length by
                     cap-trapper. cDNA went through one round of normalization
                     to Rot = 20.0 and subtraction to Rot = 459.0. Second
                     strand cDNA was prepared with the primer adapter of
                     sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCC
                     3']. cDNA was cleaved with XhoI and BamHI. Vector: a
                     modified pBluescript KS(+) after bulk excision from Lambda
```

FLC I."
BASE COUNT 186 a 162 c 142 g 142 t
ORIGIN

Query Match 21.6%; Score 284.4; DB 10; Length 632;
Best Local Similarity 67.0%; Pred. No. 1.9e-33;
Matches 488; Conservative 0; Mismatches 141; Indels 99; Gaps 2;

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Qy    220 ACAGTCACACTTGCAACCATGATGCCTAAACATTGCTTTCTAGGCTTCCTCATCAGTTTC 279
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Db      4 ACAAGCACACTTGCAACCATGATGCCTAAGCATTGCCTTCTAGGTCTCCTCATCA---TA 60

Qy    280 TTCCTTACTGGTGTAGCAGGAACTCAGTCAACGCATGAGTCTCTGAAGCCTCAGAGGGTA 339
           || | |   ||| | ||| ||  ||  || | | ||  ||||||| ||| |||| |||
Db     61 CTCTTGAGCAGTGCAACAGAAATACAACCAGCTCGTGTATCTCTGACGCCCCAGAAGGTC 120

Qy    340 CAATTTCAGTCCCGAAATTTTCACAACATTTTGCAATGGCAGCCTGGGAGGGCACTTACT 399
          | |||||||||| |||||| ||||| |||||||| |||||  | |||||  | ||  |
Db    121 CGATTTCAGTCCAGAAATTTCCACAATATTTTGCACTGGCAAGCAGGGAGCTCTCTCCCC 180

Qy    400 GGCAACAGCAGTGTCTATTTTGTGCAGTACAAAATCATGTTCTCATGCAGCATGAAAAGC 459
           |||||| |||  |||| |||||||||||||| ||
Db    181 AGCAACAACAGCATCTACTTTGTGCAGTACAAGATG---------------------- 216

Qy    460 TCTCACCAGAAGCCAAGTGGATGCTGGCAGCACATTTCTTGTAACTTCCCAGGCTGCAGA 519

Db    217 ------------------------------------------------------------ 216

Qy    520 ACATTGGCTAAATATGGACAGAGACAATGGAAAAATAAAGAAGACTGTTGGGGTACTCAA 579
                  |||||||||| |||||| || ||||||  ||||| ||||| ||
Db    217 ------------TATGGACAGAGCCAATGGGAAGATAAAGTTGACTGCTGGGGGACCACG 264

Qy    580 GAACTCTCTTGTGACCTTACCAGTGAAACCTCAGACATACAGGAACCTTATTACGGGAGG 639
          |  ||||  |||||||| |||| |||||||| ||||  | | || |  ||||||||||||
Db    265 GCGCTCTTATGTGACCTGACCAATGAAACCTTAGACCCATACGAGCTGTATTACGGGAGG 324

Qy    640 GTGAGGGCGGCCTCGGCTGGGAGCTACTCAGAATGGAGCATGACGCCGCGGTTCACTCCC 699
          ||||  | ||||||  |||||  || |||| |  |||| || ||| || || ||||||||
Db    325 GTGATGACGGCCTGTGCTGGACGCCACTCTGCCTGGACCAGGACACCCCGCTTCACTCCA 384

Qy    700 TGGTGGGAAACAAAAATAGATCCTCCAGTCATGAATATAACCCAAGTCAATGGCTCTTTG 759
          |||||||||||||||| |||||||||| ||| ||| |||||||| ||| || |  ||||||
Db    385 TGGTGGGAAACAAAACTAGATCCTCCGGTCGTGACTATAACCCGAGTTAACGCATCTTTG 444

Qy    760 TTGGTAATTCTCCATGCTCCAAATTTACCATATAGATACCAAAAGGAAAAAAATGTATCT 819
            |||  |||||| | ||||| | || ||| ||||| ||||||  | ||||||| |||
Db    445 CGGGTGCTTCTCCGTCCTCCAGAGTTGCCAAATAGAAACCAAAGTGGAAAAAATGCATCC 504

Qy    820 ATAGAAGATTACTATGAACTACTATACCGAGTTTTTATAATTAACAATTCACTAGAAAAG 879
          || |||  |||||| |   || ||||| |||||||| | ||| ||||||||||||| |||
Db    505 ATGGAAACTTACTACGGCTTAGTATACAGAGTTTTCACAATCAACAATTCACTAGAGAAG 564

Qy    880 GAGCAAAAGGTTTATGAAGGGGCTCACAGAGCGGTTGAAATTGAAGCTCTAACACCACAC 939
          |||||||| |  |||||||  |||| ||||| |||||||||||| ||| | ||| ||
Db    565 GAGCAAAAAGCCTATGAAGGAACTCAGAGAGCTGTTGAAATTGAAGGTCTGATACCTCAT 624

Qy    940 TCCAGCTA 947
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Db    625 TCCAGCTA 632
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RESULT 3
BB222214
LOCUS BB222214 663 bp mRNA linear EST 23-OCT-2001
DEFINITION BB222214 RIKEN full-length enriched, adult male aorta and vein Mus musculus cDNA clone A530075F17 3', mRNA sequence.
ACCESSION BB222214
VERSION BB222214.2 GI:16353689
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 663)
AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.
TITLE RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
JOURNAL Unpublished (2001)
COMMENT On Jul 1, 2000 this sequence version replaced gi:8890826.
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. . 10 (11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)
Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and Hayashizaki,Y.
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

FEATURES Location/Qualifiers
source 1. .663
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="A530075F17"
/clone_lib="RIKEN full-length enriched, adult male aorta and vein"
/sex="male"
/tissue_type="aorta and vein"
/dev_stage="adult"
/lab_host="DH10B"
/note="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 459.0. Second strand cDNA was prepared with the primer adapter of

sequence [5′ GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCCC 3′]. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."

BASE COUNT 188 a 176 c 146 g 153 t
ORIGIN

Query Match 16.9%; Score 222.4; DB 10; Length 663;
Best Local Similarity 65.0%; Pred. No. 3.3e-24;
Matches 417; Conservative 0; Mismatches 126; Indels 99; Gaps 2;

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Qy    228 ACTTGCAACCATGATGCCTAAACATTGCTTTCTAGGCTTCCTCATCAGTTTCTTCCTTAC 287
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Db    121 ACTTGCAACCATGATGCCTAAGCATTGCCTTCTAGGTCTCCTCATCATACTCTTGAGCA- 179

Qy    288 TGGTGTAGCAGGAACTCAGTCAACGCATGAGTCTCTGAAGCCTCAGAGGGTACAATTTCA 347
          ||| | ||| ||  ||  || | | ||  ||||||| ||| |||| ||| | ||||||
Db    180 --GTGCAACAGAAATACAACCAGCTCGTGTATCTCTGACGCCCCAGAAGGTCCGATTTCA 237

Qy    348 GTCCCGAAATTTTCACAACATTTTGCAATGGCAGCCTGGGAGGGCACTTACTGGCAACAG 407
          |||| ||||||| ||||| |||||||| ||||| | ||||| | || | ||||||
Db    238 GTCCAGAAATTTCCACAATATTTTGCACTGGCAAGCAGGGAGCTCTCTCCCCAGCAACAA 297

Qy    408 CAGTGTCTATTTTGTGCAGTACAAAATCATGTTCTCATGCAGCATGAAAAGCTCTCACCA 467
          |||  |||| |||||||||||||| ||
Db    298 CAGCATCTACTTTGTGCAGTACAAGATG---------------------------------- 325

Qy    468 GAAGCCAAGTGGATGCTGGCAGCACATTTCTTGTAACTTCCCAGGCTGCAGAACATTGGC 527

Db    326 ------------------------------------------------------------ 325

Qy    528 TAAATATGGACAGAGACAATGGAAAAATAAAGAAGACTGTTGGGGTACTCAAGAACTCTC 587
          |||||||||| |||||| || |||||| ||||| ||||| ||    | ||||
Db    326 ----TATGGACAGAGCCAATGGGAAGATAAAGTTGACTGCTGGGGGACCACGGCGCTCTT 381

Qy    588 TTGTGACCTTACCAGTGAAACCTCAGACATACAGGAACCTTATTACGGGAGGGTGAGGGC 647
          |||||||| |||| |||||||| ||||  | | || |  ||||||||||||||| | |
Db    382 CTGTGACCTGACCAATGAAACCTTAGACCCATACGAGCTGTATTACGGGAGGGTGATGAC 441

Qy    648 GGCCTCGGCTGGGAGCTACTCAGAATGGAGCATGACGCCGCGGTTCACTCCCTGGTGGGA 707
          |||||  |||||  || |||| |  |||| || ||| || || |||||||| ||||||||
Db    442 GGCCTGTGCTGGACGCCACTCTGCCTGGACCAGGACACCCCGCTTCACTCCATGGTGGGA 501

Qy    708 AACAAAAATAGATCCTCCAGTCATGAATATAACCCAAGTCAATGGCTCTTTGTTGGTAAT 767
          ||||||| |||||||||| ||| ||| |||||||| ||| || |  ||||||  |||  |
Db    502 AACAAAACTAGATCCTCCGGTCGTGACTATAACCCGAGTTAACGCATCTTTGCGGGTGCT 561

Qy    768 TCTCCATGCTCCAAATTTACCATATAGATACCAAAAGGAAAAAAATGTATCTATAGAAGA 827
          ||||| | ||||| | || ||| ||||| ||||||  | |||||||| ||| || |||
Db    562 TCTCCGTCCTCCAGAGTTGCCAAATAGAAACCAAAGTGGAAAAAATGCATCCATGGAAAC 621

Qy    828 TTACTATGAACTACTATACCGAGTTTTTATAATTAACAATTC 869
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Db    622 TTACTACGGCTTAGTATACAGAGTTTTCACAATCAACAATTC 663
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RESULT 4
BB637530
LOCUS BB637530 572 bp mRNA linear EST 26-OCT-2001
DEFINITION BB637530 RIKEN full-length enriched, adult male aorta and vein Mus musculus cDNA clone A530082J17 5′, mRNA sequence.
ACCESSION BB637530
VERSION BB637530.1 GI:16473311
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 572)
AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.
TITLE RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
JOURNAL Unpublished (2001)
COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. . 10 (11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)
Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and Hayashizaki,Y.
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
e mouse tissues.
FEATURES Location/Qualifiers
source 1. .572
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="A530082J17"
/clone_lib="RIKEN full-length enriched, adult male aorta and vein"
/sex="male"
/tissue_type="aorta and vein"
/dev_stage="adult"
/lab_host="DH10B"
/note="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5′ GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3′], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 459.0. Second strand cDNA was prepared with the primer adapter of sequence [5′ GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCCC 3′]. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."
BASE COUNT 167 a 147 c 154 g 102 t 2 others
ORIGIN

Query Match 12.1%; Score 160; DB 10; Length 572;
Best Local Similarity 69.2%; Pred. No. 7.5e-15;
Matches 231; Conservative 0; Mismatches 102; Indels 1; Gaps 1;

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Qy     532 TATGGACAGAGACAATGGAAAAATAAAGAAGACTGTTGGGGTACTCAAGAACTCTCTTGT 591
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Db     239 TATGGACAGAGCCAGTGGGAAGATCAAGCATAATGCTGGGGGACGACGGCGCTCTGCTGG 298

Qy     592 GACCTTACCAGTGAAACCTCAGACATACAGGAACCTTATTACGGGAGGGTGAGGGCGGCC 651
           ||||| |||| |||||||| |||| | |  | | |||||||||||||| || | ||| |
Db     299 GACCTGACCAATGAAACCTTAGACCCATACCACCTGTATTACGGGAGGGGGATGACGGTC 358

Qy     652 TCGGCTGGGAGCTACTCAGAATGGAGCATGACGCCGCGGTTCACTCCCTGGTGGGAAACA 711
           |  |||||   | |||| |  |||| || ||| ||  | || ||||| ||| |||||||||
Db     359 TGTGCTGGACCCCACTCTGGGTGGACCACGACACCCGGCTTTACTCCATGGAGGGAAACA 418

Qy     712 AAAATAGATCCTCCAGTCATGAATATAACCCAAGTCAATGGCTCTTTGTTGGTAATTCTC 771
           ||| || |  || | ||| ||| |||||||| ||| || |  ||||||  |||  |||||
Db     419 AAACTAAAAGCTGCGGTCGTGACTATAACCCGAGTGAACGCATCTTTGCGGGTGCTTCTC 478

Qy     772 CATGCTCCAAATTTACCATATAGATACCAAAAGGAAAAAAATGTATCTATAGAAGATTAC 831
           |   | ||||| |  ||| | | | ||| ||  | |||||| | |||  | |||  ||||
Db     479 CGNACCCCAAAGTNGCCAAAGACAAACCGAAGAGGAAAAAAGGCATCCCTGGAAACTTAC 538

Qy     832 TATGAACTACTATACCGAGTTTTTATAATTAACA 865
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RESULT 5
BE809214
LOCUS BE809214 494 bp mRNA linear EST 25-APR-2001
DEFINITION 214604 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BE809214
VERSION BE809214.1 GI:10240317
KEYWORDS EST.
SOURCE cow.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 494)
AUTHORS Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T., Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett ,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G., Pertea,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and Keele,J.W.
TITLE Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle
JOURNAL Genome Res. 11 (4), 626-630 (2001)
MEDLINE 21180013
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.
PCR PRimers
FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
Plate: 71 row: O column: 5
Seq primer: ATTTAGGTGACACTATAG.
FEATURES Location/Qualifiers
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/db_xref="taxon:9913"
/clone_lib="MARC 2BOV"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI; Library made from pooled tissue from testis, thymus, semitendonosus muscle, longissimus muscle, pancreas, adrenal, and endometrium."

BASE COUNT 176 a 89 c 112 g 117 t
ORIGIN

Query Match 9.4%; Score 124.2; DB 12; Length 494;
Best Local Similarity 79.5%; Pred. No. 1.8e-09;
Matches 147; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

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           |||  |||||| ||||||| ||||||||||||||   ||| ||||| | || |||  |||
Db     294 CTAGGTATGGAGAGAGACAGTGGAAAAATAAAGAGACCTGCTGGGGGATTCGAGAGTTCT 353

Qy     587 CTTGTGACCTTACCAGTGAAACCTCAGACATACAGGAACCTTATTACGGGAGGGTGAGGG 646
             |||||||||||| |||||| ||||| |||  |||||||||||. ||||| |||| |
Db     354 TCTGTGACCTTACCAATGAAACATCAGATATATGGGAACCTTATTATGGGAGAGTGAAGA 413

Qy     647 CGGCCTCGGCTGGGAGCTACTCAGAATGGAGCATGACGCCGCGGTTCACTCCCTGGTGGG 706
           | ||   |||||||| | ||||||  |||| |||||| | ||||||||  ||| |||||||
Db     414 CAGCTCTGGCTGGGATCCACTCAGGCTGGACCATGACACAGCGGTTCATTCCATGGTGGG 473

Qy     707 AAACA 711
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Db     474 AAAGA 478
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RESULT 6
BH117626/c
LOCUS BH117626 548 bp DNA linear GSS 19-JUL-2001
DEFINITION RPCI-24-253I22.TV RPCI-24 Mus musculus genomic clone RPCI-24-253I22 , DNA sequence.
ACCESSION BH117626
VERSION BH117626.1 GI:14959077
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 548)
AUTHORS Zhao,S., Nierman,W., Malek,J., Shatsman,S., Akinret,B., Levins,M., Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A., Gebregeorgis,E., Russell,D., de Jong,P. and Fraser,C.M.
TITLE Mouse BAC End Sequences from Library RPCI-24
JOURNAL Unpublished (1999)
COMMENT Other_GSSs: RPCI-24-253I22.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-24. For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end page: http://ww .tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 253 row: I column: 22
Seq primer: T7
Class: BAC ends.
FEATURES Location/Qualifiers
source 1. .548
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-24-253I22"
/clone_lib="RPCI-24"
/sex="Male"
/cell_type="Spleen/Brain"
/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1; RPCI-24 Mouse BAC Library produced by Pieter de Jong. The library was cloned in the pTARBAC1 cloning vector at the BamH1 sites using MboI partially digested male C57BL/6J DNA."
BASE COUNT 182 a 85 c 100 g 181 t

```
ORIGIN

  Query Match              8.1%;  Score 106.2;  DB 17;  Length 548;
  Best Local Similarity   75.4%;  Pred. No. 8.1e-07;
  Matches  132;  Conservative    0;  Mismatches   43;  Indels    0;  Gaps    0;

Qy     708 AACAAAAATAGATCCTCCAGTCATGAATATAACCCAAGTCAATGGCTCTTTGTTGGTAAT 767
           | ||||| |||||||||| ||| ||| |||||||| ||| || |  ||||||  |||  |
Db     229 AGCAAAACTAGATCCTCCGGTCGTGACTATAACCCGAGTTAACGCATCTTTGCGGGTGCT 170

Qy     768 TCTCCATGCTCCAAATTTACCATATAGATACCAAAAGGAAAAAAATGTATCTATAGAAGA 827
           |  |  | ||||| | || ||| ||||| ||||||  | |||||||| ||| || |||
Db     169 TAACAGTCCTCCAGAGTTGCCAAATAGAAACCAAAGTGGAAAAAATGCATCCATGGAAAC 110

Qy     828 TTACTATGAACTACTATACCGAGTTTTTATAATTAACAATTCACTAGAAAAGGAG 882
           |||||| |   || |||| |||||| | ||| |||||||||||||| |||| |
Db     109 TTACTACGGCTTAGTATACAGAGTTTTCACAATCAACAATTCACTAGAGAAGGTG 55


RESULT 7
AZ722045/c
LOCUS       AZ722045                 645 bp    DNA     linear   GSS 24-JAN-2001
DEFINITION  RPCI-24-140H15.TV RPCI-24 Mus musculus genomic clone RPCI-24-140H15
            , DNA sequence.
ACCESSION   AZ722045
VERSION     AZ722045.1  GI:12465335
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 645)
  AUTHORS   Zhao,S., Nierman,W., Malek,J., Shatsman,S., Akinret,B., Levins,M.,
            Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A., Gebregeorgis,E.,
            Russell,D., de Jong,P. and Fraser,C.M.
  TITLE     Mouse BAC End Sequences from Library RPCI-24
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Shaying Zhao
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: szhao@tigr.org
            Clones are derived from the mouse BAC library RPCI-24. For BAC
            library availability, please contact Pieter de Jong
            (pdejong@mail.cho.org). Clones may be purchased from BACPAC
            Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end
            page: http://ww .tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
            Plate: 140  row: H  column: 15
            Seq primer: T7
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .645
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="RPCI-24-140H15"
                     /clone_lib="RPCI-24"
                     /sex="Male"
                     /cell_type="Spleen/Brain"
                     /note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
                     RPCI-24 Mouse BAC Library produced by Pieter de Jong. The
                     library was  cloned in the pTARBAC1 cloning vector at the
                     BamH1 sites using MboI  partially digested male C57BL/6J
                     DNA."
BASE COUNT      191 a    156 c    121 g    177 t
ORIGIN

  Query Match              6.4%;  Score 84.6;  DB 17;  Length 645;
  Best Local Similarity   73.5%;  Pred. No. 0.0012;
  Matches  108;  Conservative    0;  Mismatches   39;  Indels    0;  Gaps    0;

Qy     288 TGGTGTAGCAGGAACTCAGTCAACGCATGAGTCTCTGAAGCCTCAGAGGGTACAATTTCA 347
           || ||    || ||  ||  || | | ||  ||||||| ||| |||| ||| | ||||||
Db     642 TGCTGCCTTAGAAATACAACCAGCTCGTGTATCTCTGACGCCCCAGAAGGTCCGATTTCA 583

Qy     348 GTCCCGAAATTTTCACAACATTTTGCAATGGCAGCCTGGGAGGGCACTTACTGGCAACAG 407
           |||| ||||||| ||||| |||||||| |||||  | |||||  | ||  |  ||||||
Db     582 GTCCAGAAATTTCCACAATATTTTGCACTGGCAAGCAGGGAGCTCTCTCCCCAGCAACAA 523

Qy     408 CAGTGTCTATTTTGTGCAGTACAAAAT 434
           |||  |||| ||||||||||||||| ||
Db     522 CAGCATCTACTTTGTGCAGTACAAGAT 496


RESULT 8
AW833620/c
LOCUS       AW833620                 583 bp    mRNA    linear   EST 18-MAY-2000
DEFINITION  QV4-TT0008-161199-033-e05 TT0008 Homo sapiens cDNA, mRNA sequence.
ACCESSION   AW833620
VERSION     AW833620.1  GI:7927594
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 583)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=&t2=QV4-TT0008-161
            199-033-e05&t3=1999-11-16&t4=1)
            Seq primer: puc 18 forward
            High quality sequence stop: 578.
FEATURES             Location/Qualifiers
     source          1. .583
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="TT0008"
                     /dev_stage="Adult"
                     /note="Organ: testis; Vector: puc18; Site_1: SmaI; Site_2:
                     SmaI; A mini-library was made by cloning products derived
                     from  ORESTES PCR (U.S. Letters Patent application No. 196
                     ,716 -  Ludwig Institute for Cancer Research) profiles
                     into  the pUC 18 vector. Reverse transcription of tissue
                     mRNA and cDNA amplification were performed under low
                     stringency conditions."
BASE COUNT      173 a    129 c    123 g    158 t
ORIGIN

  Query Match              6.1%;  Score 81;  DB 10;  Length 583;
  Best Local Similarity   89.7%;  Pred. No. 0.0045;
  Matches   87;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy     288 TGGTGTAGCAGGAACTCAGTCAACGCATGAGTCTCTGAAGCCTCAGAGGGTACAATTTCA 347
           || | |   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     100 TGTTATCTTAGGAACTCAGTCAACGCATGAGTCTCTGAAGCCTCAGAGGGTACAATTTCA 41
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Qy     348 GTCCCGAAATTTTCACAACATTTTGCAATGGCAGCCT 384
           ||||||||||||||||||||||||||| ||    |||
Db      40 GTCCCGAAATTTTCACAACATTTTGCACTGCACTCCT 4


RESULT 9
AL513907/c
LOCUS       AL513907                311 bp    mRNA    linear   EST 13-FEB-2001
DEFINITION  AL513907 LTI_NFL006_PL2 Homo sapiens cDNA clone CL0BA006ZC11 3
            prime, mRNA sequence.
ACCESSION   AL513907
VERSION     AL513907.1  GI:12777401
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 311)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES             Location/Qualifiers
     source          1. .311
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="CL0BA006ZC11"
                     /clone_lib="LTI_NFL006_PL2"
                     /tissue_type="placenta"
                     /note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
                     was primed with a NotI-oligo(dT) primer.  Five prime end
                     enriched, double-stranded cDNA was digested with Not I and
                     cloned into the Not I and Eco RV sites of the pCMVSPORT 6
                     vector. Library was normalized. Library was constructed by
                     Life Technologies. Contact : Feng Liang Life Technologies,
                     a division of Invitrogen 9800 Medical Center Drive
                     Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
                     Email : fliang@lifetech.com URL :
                     http://fulllength.invitrogen.com"
BASE COUNT      121 a      5 c      4 g    162 t     19 others
ORIGIN

  Query Match             5.9%;  Score 77.4;  DB 9;  Length 311;
  Best Local Similarity   55.8%;  Pred. No. 0.023;
  Matches  120;  Conservative   12;  Mismatches   83;  Indels    0;  Gaps    0;

     1104 TCTTATTTAAAATTGTTTTTGTATTTTCTTAAAGCAATATTCACTGTTACACCTTGGGGA 1163
          | || |||    || ||||| | |||| ||    :  | :|| :: |: :  :||
Db     283 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 224

Qy    1164 CTTCTTTGTTTATCCATTCTTTTATCCTTTATATTTCATTTGTAAACTATATTTGAACGA 1223
           || ||| ||| |   || |||| |  ||| | :||  ||| |:||  | |||| ::  |
Db     223 TTTTTTTTTTTTTTTTTTTTTTTTTTTWTTTTTTWTTTTTTTTTWAATAAAATTTWWWWAA 164

Qy    1224 CATTCCCCCCCGAAAAATTGAAATGTAAAGATGAGGCAGAGAATAAAGTGTTCTATGAAAA 1283
           :         |||||   |||   ||| |  |   | | || |||       |  ||||
Db     163 AWAAAAAAWAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 104

Qy    1284 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1318
           ||||||||||||||||||||||||||||||||||
Db     103 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 69


RESULT 10
AL513907
LOCUS       AL513907                311 bp    mRNA    linear   EST 13-FEB-2001
DEFINITION  AL513907 LTI_NFL006_PL2 Homo sapiens cDNA clone CL0BA006ZC11 3
            prime, mRNA sequence.
ACCESSION   AL513907
VERSION     AL513907.1  GI:12777401
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 311)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES             Location/Qualifiers
     source          1. .311
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="CL0BA006ZC11"
                     /clone_lib="LTI_NFL006_PL2"
                     /tissue_type="placenta"
                     /note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
                     was primed with a NotI-oligo(dT) primer.  Five prime end
                     enriched, double-stranded cDNA was digested with Not I and
                     cloned into the Not I and Eco RV sites of the pCMVSPORT 6
                     vector. Library was normalized. Library was constructed by
                     Life Technologies. Contact : Feng Liang Life Technologies,
                     a division of Invitrogen 9800 Medical Center Drive
                     Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
                     Email : fliang@lifetech.com URL :
                     http://fulllength.invitrogen.com"
BASE COUNT      121 a      5 c      4 g    162 t     19 others
ORIGIN

  Query Match             5.8%;  Score 77;  DB 9;  Length 311;
  Best Local Similarity   55.3%;  Pred. No. 0.026;
  Matches  119;  Conservative   13;  Mismatches   83;  Indels    0;  Gaps    0;

Qy    1104 TCTTATTTAAAATTGTTTTTGTATTTTCTTAAAGCAATATTCACTGTTACACCTTGGGGA 1163
           | || |||    || ||||| | |||| ||       | ||   | ||     ||
Db      67 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 126

Qy    1164 CTTCTTTGTTTATCCATTCTTTTATCCTTTATATTTCATTTGTAAACTATATTTGAACGA 1223
            || ||| ||| |   || |||| |  |:| | ||:  |:: :||| | ||||: ||  |
Db     127 TTTTTTTTTTTTTTTTTTTTTTTTTTTWTTTTTTWTTTWWWWAAATTTTATTWAAAAAA 186

Qy    1224 CATTCCCCCCCGAAAAATTGAAATGTAAAGATGAGGCAGAGAATAAAGTGTTCTATGAAAA 1283
            | :       |||||   |||   ||| | ,|   | | || |:|: :    : ||:||
Db     187 AAAWAAAAAAWAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAARARRRRAGRRAGARAA 246

Qy    1284 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1318
           ||:|||||||||||||||||||||||||||||||||
Db     247 AARAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 281


RESULT 11
AL513951/c
LOCUS       AL513951                454 bp    mRNA    linear   EST 13-FEB-2001
DEFINITION  AL513951 LTI_NFL006_PL2 Homo sapiens cDNA clone CL0BA010ZD12 3
            prime, mRNA sequence.
ACCESSION   AL513951
VERSION     AL513951.1  GI:12777445
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 454)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
```

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          Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES             Location/Qualifiers
     source          1. .454
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="CL0BA010ZD12"
                     /clone_lib="LTI_NFL006_PL2"
                     /tissue_type="placenta"
                     /note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
                     was primed with a NotI-oligo(dT) primer.  Five prime end
                     enriched, double-stranded cDNA was digested with Not I and
                     cloned into the Not I and Eco RV sites of the pCMVSPORT 6
                     vector. Library was normalized. Library was constructed by
                     Life Technologies. Contact : Feng Liang Life Technologies,
                     a division of Invitrogen 9800 Medical Center Drive
                     Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
                     Email : fliang@lifetech.com URL :
                     http://fulllength.invitrogen.com"
BASE COUNT      226 a     33 c     26 g    127 t     42 others
ORIGIN

  Query Match              5.8%;  Score 76.2;  DB 9;  Length 454;
  Best Local Similarity   53.1%;  Pred. No. 0.027;
  Matches  120;  Conservative   15;  Mismatches   91;  Indels    0;  Gaps    0;

Qy    1093 TGTTTGAAGGATCTTATTTAAAATTGTTTTTGTATTTTCTTAAAGCAATATTCACTGTTA 1152
           | ||::  || : || |||    || ||||| | |||||:|      : :|   | |
Db     277 TTTTKKGGGGGKTTTTTTTTTTTTTTTTTTTTTTTTTCYTYYYTTTTKKKTTTTTTTCC 218

Qy    1153 CACCTTGGGGACTTCTTTGTTTATCCATTCTTTTATCCTTTATATTTCATTTGTAAACTA 1212
           | ::||      || ::|:||| |   || |||| :::||| | |||  ||| |    |
Db     217 CCYYTTTTTTTTTTTTYYTKTTTTTTTTTTTTTTTTYYYYTTTTTTTTTTTTTTTTTTTT 158

Qy    1213 TATTTGAACGACATTCCCCCCGAAAAATTGAAATGTAAAGATGAGGCAGAGAATAAAGTG 1272
           | |||        ||       |||||   |||   ||| |  |   | | || |||
Db     157 TTTTTTTTTTTTTTTTKGNNNAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 98

Qy    1273 TTCTATGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1318
             |  |||||||||||||||||||||||||||||||||||||||||||||:
Db      97 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAM 52


RESULT 12
AL514919/c
LOCUS       AL514919                304 bp    mRNA    linear   EST 13-FEB-2001
DEFINITION  AL514919 LTI_NFL006_PL2 Homo sapiens cDNA clone CL0BB012ZF06 3
            prime, mRNA sequence.
ACCESSION   AL514919
VERSION     AL514919.1  GI:12778412
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES             Location/Qualifiers
     source          1. .304
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="CL0BB012ZF06"
                     /clone_lib="LTI_NFL006_PL2"
                     /tissue_type="placenta"
                     /note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
                     was primed with a NotI-oligo(dT) primer.  Five prime end
                     enriched, double-stranded cDNA was digested with Not I and
                     cloned into the Not I and Eco RV sites of the pCMVSPORT 6
                     vector. Library was normalized. Library was constructed by
                     Life Technologies. Contact : Feng Liang Life Technologies,
                     a division of Invitrogen 9800 Medical Center Drive
                     Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
                     Email : fliang@lifetech.com URL :
                     http://fulllength.invitrogen.com"
BASE COUNT      134 a      5 c      8 g    151 t      6 others
ORIGIN

  Query Match              5.8%;  Score 75.8;  DB 9;  Length 304;
  Best Local Similarity   58.1%;  Pred. No. 0.04;
  Matches  125;  Conservative    4;  Mismatches   86;  Indels    0;  Gaps    0;

Qy    1104 TCTTATTTAAAATTGTTTTTGTATTTTCTTAAAGCAATATTCACTGTTACACCTTGGGGA 1163
           | || |||    || ||||| | |||| ||       | ||   | ||     ||
Db     276 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTKKTTTTTTTTTTTTTT 217

Qy    1164 CTTCTTTGTTTATCCATTCTTTTATCCTTTATATTTCATTTGTAAACTATATTTGAACGA 1223
            || ||| ||| |   || |||| |  ||| | |||  ||  |||  ||||||  |||
Db     216 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTATTAATTTATATTAAAACCC 157

Qy    1224 CATTCCCCCCGAAAAATTGAAATGTAAAGATGAGGCAGAGAATAAAGTGTTCTATGAAAA 1283
            |  | :  : :||||   :||   ||| |  |   | | || |||       |  ||||
Db     156 AAAACAMAAMCMAAAAAAAWAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 97

Qy    1284 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1318
           ||||||||||||||||||||||||||||||||||
Db      96 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 62


RESULT 13
AL513977/c
LOCUS       AL513977                319 bp    mRNA    linear   EST 13-FEB-2001
DEFINITION  AL513977 LTI_NFL006_PL2 Homo sapiens cDNA clone CL0BA011ZF09 3
            prime, mRNA sequence.
ACCESSION   AL513977
VERSION     AL513977.1  GI:12777471
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 319)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES             Location/Qualifiers
     source          1. .319
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="CL0BA011ZF09"
                     /clone_lib="LTI_NFL006_PL2"
                     /tissue_type="placenta"
                     /note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
                     was primed with a NotI-oligo(dT) primer.  Five prime end
                     enriched, double-stranded cDNA was digested with Not I and
                     cloned into the Not I and Eco RV sites of the pCMVSPORT 6
                     vector. Library was normalized. Library was constructed by
                     Life Technologies. Contact : Feng Liang Life Technologies,
                     a division of Invitrogen 9800 Medical Center Drive
                     Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
                     Email : fliang@lifetech.com URL :
                     http://fulllength.invitrogen.com"
BASE COUNT      150 a     12 c      7 g    148 t      2 others
ORIGIN

  Query Match              5.7%;  Score 75.4;  DB 9;  Length 319;
  Best Local Similarity   59.1%;  Pred. No. 0.044;
  Matches  127;  Conservative    1;  Mismatches   87;  Indels    0;  Gaps    0;
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Qy   1104 TCTTATTTAAAATTGTTTTTGTATTTTCTTAAAGCAATATTCACTGTTACACCTTGGGGA 1163
          | || |||    || ||||| ||||||  |||| |  | ||   | ||     ||
Db    263 TTTTTTTTTTTTTTTTTTTTATATTTTATAAAACCCTTTTTTTTTTTTTTTTTTTTT 204

Qy   1164 CTTCTTTGTTTATCCATTCTTTTATCCTTTATATTTCATTTGTAAACTATATTTGAACGA 1223
            || ||| ||| :   || |||| |  ||| | |||  ||| |    | | |||
Db    203 TTTTTTTTTTTGKTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 144

Qy   1224 CATTCCCCCCGAAAAATTGAAATGTAAAGATGAGGCAGAGAATAAAGTGTTCTATGAAAA 1283
            ||       ||||||  |||   ||| |  |   | | || |||    |  |  ||||
Db    143 TTTTTAAAAAAAAAAATATAAAAAAAAAAAAATAAAAAAAAAAAAAAAAAAATAAAAAAAAA 84

Qy   1284 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1318
          ||||||||||||||||||||||||||||||||||
Db     83 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 49
```

RESULT 14
AL515373/c
LOCUS AL515373 365 bp mRNA linear EST 13-FEB-2001
DEFINITION AL515373 LTI_NFL006_PL2 Homo sapiens cDNA clone CL0BB017ZD11 3 prime, mRNA sequence.
ACCESSION AL515373
VERSION AL515373.1 GI:12778866
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 365)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES Location/Qualifiers
source 1. .365
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/db_xref="taxon:9606"
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BASE COUNT 100 a 5 c 6 g 230 t 24 others
ORIGIN

Query Match 5.7%; Score 75.2; DB 9; Length 365;
Best Local Similarity 53.8%; Pred. No. 0.044;
Matches 113; Conservative 17; Mismatches 80; Indels 0; Gaps 0;

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RESULT 15
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LOCUS AL513809 503 bp mRNA linear EST 13-FEB-2001
DEFINITION AL513809 LTI_NFL006_PL2 Homo sapiens cDNA clone CL0BA009ZF09 3 prime, mRNA sequence.
ACCESSION AL513809
VERSION AL513809.1 GI:12777303
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 503)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES Location/Qualifiers
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/clone_lib="LTI_NFL006_PL2"
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/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"
BASE COUNT 138 a 144 c 4 g 133 t 84 others
ORIGIN

Query Match 5.6%; Score 74.4; DB 9; Length 503;
Best Local Similarity 43.4%; Pred. No. 0.048;
Matches 98; Conservative 45; Mismatches 83; Indels 0; Gaps 0;

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Job time : 1977 secs

GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: December 22, 2002, 07:44:21 ; Search time 55 Seconds
(without alignments)
7349.090 Million cell updates/sec

Title: US-09-964-994-1
Perfect score: 1318
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

[redacted]l number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	69.2	5.3	1659	2	US-08-943-087-45	Sequence 45, Appl
2	68.6	5.2	1659	2	US-08-943-087-13	Sequence 13, Appl
3	68.6	5.2	1659	2	US-08-943-087-31	Sequence 31, Appl
4	68	5.2	1659	2	US-08-943-087-19	Sequence 19, Appl
5	67.8	5.1	663	2	US-08-943-087-53	Sequence 53, Appl
6	67	5.1	663	2	US-08-943-087-49	Sequence 49, Appl
7	67	5.1	663	2	US-08-943-087-51	Sequence 51, Appl
8	67	5.1	1659	2	US-08-943-087-15	Sequence 15, Appl
9	67	5.1	1659	2	US-08-943-087-17	Sequence 17, Appl
10	67	5.1	1659	2	US-08-943-087-23	Sequence 23, Appl
11	67	5.1	3516	2	US-08-943-087-1	Sequence 1, Appli
12	66.8	5.1	1659	2	US-08-943-087-25	Sequence 25, Appl
13	66.4	5.0	1659	2	US-08-943-087-21	Sequence 21, Appl
14	65.4	5.0	663	2	US-08-943-087-57	Sequence 57, Appl
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16	65.4	5.0	1659	2	US-08-943-087-39	Sequence 39, Appl
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19	63.8	4.8	663	2	US-08-943-087-55	Sequence 55, Appl
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44	53.6	4.1	2852	3	US-09-027-137-2	Sequence 2, Appli
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ALIGNMENTS

RESULT 1
US-08-943-087-45
; Sequence 45, Application US/08943087
; Patent No. 5945511
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Farrah, Theresa M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,087
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/803,305
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-24C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1659 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...1659

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;      OTHER INFORMATION:
US-08-943-087-45

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; Sequence 13, Application US/08943087
; Patent No. 5945511
;  GENERAL INFORMATION:
;    APPLICANT:  Lok, Si
;    APPLICANT:  Kho, Choon J.
;    APPLICANT:  Jelmberg, Anna C.
;    APPLICANT:  Adams, Robyn L.
;    APPLICANT:  Whitmore, Theodore E.
;    APPLICANT:  Farrah, Theresa M.
;    TITLE OF INVENTION:  CYTOKINE RECEPTOR
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ZymoGenetics, Inc.
;      STREET:  1201 Eastlake Avenue East
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98102
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/943,087
;      FILING DATE:
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/803,305
;      FILING DATE:  20-FEB-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lunn, Paul G
;      REGISTRATION NUMBER:  32,743
;      REFERENCE/DOCKET NUMBER:  96-24C1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206-442-6627
;      TELEFAX:  206-442-6678
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1659 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  1...1659
;      OTHER INFORMATION:
US-08-943-087-13

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RESULT 3
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; Patent No. 5945511
;  GENERAL INFORMATION:
;    APPLICANT:  Lok, Si
;    APPLICANT:  Kho, Choon J.
;    APPLICANT:  Jelmberg, Anna C.
;    APPLICANT:  Adams, Robyn L.
;    APPLICANT:  Whitmore, Theodore E.
;    APPLICANT:  Farrah, Theresa M.
;    TITLE OF INVENTION:  CYTOKINE RECEPTOR
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ZymoGenetics, Inc.
;      STREET:  1201 Eastlake Avenue East
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98102
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/943,087
;      FILING DATE:
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/803,305
;      FILING DATE:  20-FEB-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lunn, Paul G
;      REGISTRATION NUMBER:  32,743
;      REFERENCE/DOCKET NUMBER:  96-24C1
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;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  206-442-6627
;       TELEFAX:  206-442-6678
;       TELEX:
;   INFORMATION FOR SEQ ID NO:  31:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1659 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
;     FEATURE:
;       NAME/KEY:  Coding Sequence
;       LOCATION:  1...1659
;       OTHER INFORMATION:
US-08-943-087-31

  Query Match             5.2%;  Score 68.6;  DB 2;  Length 1659;
  Best Local Similarity   51.8%;  Pred. No. 4.4e-07;
  Matches  155;  Conservative    0;  Mismatches  144;  Indels    0;  Gaps    0;

Qy      529 AAATATGGACAGAGACAATGGAAAAATAAAGAAGACTGTTGGGGTACTCAAGAACTCTCT 588
            | |||||| || |   |||||   ||||||  ||| ||  |   ||   |   |  ||
Db      223 ATATATGGGCAAAAGAAATGGCTGAATAAATCAGAATGCAGAAATATCAATAGAACCTAC 282

Qy      589 TGTGACCTTACCAGTGAAACCTCAGACATACAGGAACCTTATTACGGGAGGGTGAGGGCG 648
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Db      283 TGTGATCTTTCTGCTGAAACTTCTGACTACGAACACCAGTATTATGCCAAAGTTAAGGCC 342

Qy      649 GCCTCGGCTGGGAGCTACTCAGAATGGAGCATGACGCCGCGGTTCACTCCCTGGTGGGAA 708
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Db      343 ATTTGGGGAACAAAGTGTTCCAAATGGGCTGAAAGTGGACGGTTCTATCCTTTTTTGGAA 402

Qy      709 ACAAAAATAGATCCTCCAGTCATGAATATAACCCAAGTCAATGGCTCTTTGTTGGTAATT 768
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Db      463 CTGACAGCTCCAGAGAAGTGGAAGAGAAATCCAGAAGACCTTCCTGTTTCCATGCAACA 521


RESULT 4
US-08-943-087-19
; Sequence 19, Application US/08943087
; Patent No. 5945511
;  GENERAL INFORMATION:
;    APPLICANT:  Lok, Si
;    APPLICANT:  Kho, Choon J.
;    APPLICANT:  Jelmberg, Anna C.
;    APPLICANT:  Adams, Robyn L.
;    APPLICANT:  Whitmore, Theodore E.
;    APPLICANT:  Farrah, Theresa M.
;    TITLE OF INVENTION:  CYTOKINE RECEPTOR
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ZymoGenetics, Inc.
;      STREET:  1201 Eastlake Avenue East
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98102
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/943,087
;      FILING DATE:
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/803,305
;      FILING DATE:  20-FEB-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lunn, Paul G
;      REGISTRATION NUMBER:  32,743
;      REFERENCE/DOCKET NUMBER:  96-24C1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206-442-6627
;      TELEFAX:  206-442-6678
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  19:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1659 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  Coding Sequence
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US-08-943-087-19

  Query Match             5.2%;  Score 68;  DB 2;  Length 1659;
  Best Local Similarity   51.7%;  Pred. No. 6.1e-07;
  Matches  155;  Conservative    0;  Mismatches  145;  Indels    0;  Gaps    0;

Qy      528 TAAATATGGACAGAGACAATGGAAAAATAAAGAAGACTGTTGGGGTACTCAAGAACTCTC 587
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Db      222 TATATATGGGCAAAAGAAATGGCTGAATAAATCAGAGTGCAGAAATATCAATAGAACCTA 281

Qy      588 TTGTGACCTTACCAGTGAAACCTCAGACATACAGGAACCTTATTACGGGAGGGTGAGGGC 647
             |||||  |||  |   |||  ||  ||  |||     ||  |  |  |||||  |  |  || | |||
Db      282 CTGTGATCTTTCTGCTGAGACTTCTGACTACGAGCACCAGTATTATGCCAAAGTTAAGGC 341

Qy      648 GGCCTCGGCTGGGAGCTACTCAGAATGGAGCATGACGCCGCGGTTCACTCCCTGGTGGGA 707
              | ||     |  |  ||  |||||      ||      |||||   |||  |  |  ||
Db      342 CATTTGGGGAACAAAGTGTTCCAAATGGGCTGAGAGTGGACGGTTTTATCCTTTTTTAGA 401

Qy      708 AACAAAAATAGATCCTCCAGTCATGAATATAACCCAAGTCAATGGCTCTTTGTTGGTAAT 767
             |||  ||||  |  ||  ||||   ||     | ||   ||   |     ||  | |  ||  |
Db      402 GACACAAATTGGCCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTTCTGTTGT 461

Qy      768 TCTCCATGCTCCAAATTTACCATATAGATACCAAAAGGAAAAAAATGTATCTATAGAAGA 827
            ||    ||||||  |        | |||  | | | | ||||      |||  ||  ||  ||  |
Db      462 CCTGACAGCTCCAGAGAAGTGGAAGAGAAATCCAGAGGACCTTCCTGTTTCCATGCAACA 521


RESULT 5
US-08-943-087-53
; Sequence 53, Application US/08943087
; Patent No. 5945511
;  GENERAL INFORMATION:
;    APPLICANT:  Lok, Si
;    APPLICANT:  Kho, Choon J.
;    APPLICANT:  Jelmberg, Anna C.
;    APPLICANT:  Adams, Robyn L.
;    APPLICANT:  Whitmore, Theodore E.
;    APPLICANT:  Farrah, Theresa M.
;    TITLE OF INVENTION:  CYTOKINE RECEPTOR
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ZymoGenetics, Inc.
;      STREET:  1201 Eastlake Avenue East
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98102
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/08/943,087
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/803,305
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-24C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 663 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...663
; OTHER INFORMATION:
US-08-943-087-53

Query Match 5.1%; Score 67.8; DB 2; Length 663;
Best Local Similarity 51.5%; Pred. No. 5.1e-07;
Matches 156; Conservative 0; Mismatches 147; Indels 0; Gaps 0;

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Qy    531 ATATGGACAGAGACAATGGAAAAATAAAGAAGACTGTTGGGGTACTCAAGAACTCTCTTG 590
          |||||| || |   |||||   ||||||  ||| ||  |   ||   |  |  ||  ||
Db    138 ATATGGGCAAAAGAAATGGCTGAATAAATCAGAATGCAGAAATATCAATAGAACCTACTG 197

Qy    591 TGACCTTACCAGTGAAACCTCAGACATACAGGAACCTTATTACGGGAGGGTGAGGGCGGC 650
          |||  |||  |   |||||| ||  |||     |  | |  |||||  |  |  ||  | |||
Db    198 TGATCTTTCTGCTGAAACTTCTGACTACGAACACCAGTATTATGCCAAAGTTAAGGCCAT 257

Qy    651 CTCGGCTGGGAGCTACTCAGAATGGAGCATGACGCCGCGGTTCACTCCCTGGTGGGAAAC 710
            | ||      |  |  ||  |||||      |     ||||||  |||  |  |  |||||
Db    258 TTGGGGAACAAAGTGTTCCAAATGGGCTGAAAGTGGACGGTTCTATCCTTTTTTAGAAAC 317

Qy    711 AAAAATAGATCCTCCAGTCATGAATATAACCCAAGTCAATGGCTCTTTGTTGGTAATTCT 770
          | ||||  |  || ||||   ||    | ||   ||   |    ||  | |  ||  | ||
Db    318 ACAAATTGGCCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTTCTGTTGTCCT 377

Qy    771 CCATGCTCCAAATTTACCATATAGATACCAAAAGGAAAAAAATGTATCTATAGAAGATTA 830
          ||||||  |         | ||| | | | | ||      ||| || ||  || | |
Db    378 GACAGCTCCAGAGAAGTGGAAGAGAAATCCAGAAGACCTTCCTGTTTCCATGCAACAATT 437

Qy    831 CTA 833
            ||
Db    438 ATA 440
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RESULT 6
US-08-943-087-49
; Sequence 49, Application US/08943087
; Patent No. 5945511
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Farrah, Theresa M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,087
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/803,305
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-24C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 663 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...663
; OTHER INFORMATION:
US-08-943-087-49

Query Match 5.1%; Score 67; DB 2; Length 663;
Best Local Similarity 51.5%; Pred. No. 7.9e-07;
Matches 154; Conservative 0; Mismatches 145; Indels 0; Gaps 0;

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Qy    529 AAATATGGACAGAGACAATGGAAAAATAAAGAAGACTGTTGGGGTACTCAAGAACTCTCT 588
          | ||||||  || |   |||||   ||||||  ||| ||  |   ||   |  |  ||
Db    136 ATATATGGGCAAAAGAAATGGCTGAATAAATCAGAATGCAGAAATATCAATAGAACCTAC 195

Qy    589 TGTGACCTTACCAGTGAAACCTCAGACATACAGGAACCTTATTACGGGAGGGTGAGGGCG 648
          |||||  |||  |   ||||||  ||  |||     |  |  |  |||||  |  |  ||  | |||
Db    196 TGTGATCTTTCTGCTGAAACTTCTGACTACGAACACCAGTATTATGCCAAAGTTAAGGCC 255

Qy    649 GCCTCGGCTGGGAGCTACTCAGAATGGAGCATGACGCCGCGGTTCACTCCCTGGTGGGAA 708
            | ||      |  |  ||  |||||      |     ||||||  |||  |  |  |||
Db    256 ATTTGGGGAACAAAGTGTTCCAAATGGGCTGAAAGTGGACGGTTCTATCCTTTTTTAGAA 315

Qy    709 ACAAAAATAGATCCTCCAGTCATGAATATAACCCAAGTCAATGGCTCTTTGTTGGTAATT 768
          |||  ||||  |  ||  ||||   ||    | ||   ||   |    ||  |  |  ||  |
Db    316 ACACAAATTGGCCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTTCTGTTGTC 375

Qy    769 CTCCATGCTCCAAATTTACCATATAGATACCAAAAGGAAAAAAATGTATCTATAGAAGA 827
          ||    ||||||  |         | |||  |  |  |  ||      |||  ||  ||  ||  |
Db    376 CTGACAGCTCCAGAGAAGTGGAAGAGAAATCCAGAAGACCTTCCTGTTTCCATGCAACA 434
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RESULT 7
US-08-943-087-51
; Sequence 51, Application US/08943087
; Patent No. 5945511
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Farrah, Theresa M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR

```
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ZymoGenetics, Inc.
;      STREET:  1201 Eastlake Avenue East
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98102
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/943,087
;      FILING DATE:
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/803,305
;      FILING DATE:  20-FEB-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lunn, Paul G
;      REGISTRATION NUMBER:  32,743
;      REFERENCE/DOCKET NUMBER:  96-24C1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206-442-6627
;      TELEFAX:  206-442-6678
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  51:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  663 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  1...663
;      OTHER INFORMATION:
US-08-943-087-51

  Query Match             5.1%;  Score 67;  DB 2;  Length 663;
  Best Local Similarity   51.5%;  Pred. No. 7.9e-07;
  Matches  154;  Conservative    0;  Mismatches  145;  Indels    0;  Gaps    0;

Qy     529 AAATATGGACAGAGACAATGGAAAAATAAAGAAGACTGTTGGGGTACTCAAGAACTCTCT 588
           | |||||| || |   |||||  ||||||  ||| ||  |   ||   |   |  ||
Db     136 ATATATGGGCAAAAGAAATGGCTGAATAAATCAGAATGCAGAAATATCAATAGAACCTAC 195

Qy     589 TGTGACCTTACCAGTGAAACCTCAGACATACAGGAACCTTATTACGGGAGGGTGAGGGCG 648
           |||||  |||  |   ||||||  ||  |||    |  | |  |||||  |  |  || | |||
Db     196 TGTGATCTTTCTGCTGAAACTTCTGACTACGAACACCAGTATTATGCCAAAGTTAAGGCC 255

Qy     649 GCCTCGGCTGGGAGCTACTCAGAATGGAGCATGACGCCGCGGTTCACTCCCTGGTGGGAA 708
             | ||     |  |  ||  |||||      |     ||||||  |||  |  |  |||
Db     256 ATTTGGGGAACAAAGTGTTCCAAATGGGCTGAAAGTGGACGGTTCTATCCTTTTTTAGAA 315

Qy     709 ACAAAAATAGATCCTCCAGTCATGAATATAACCCAAGTCAATGGCTCTTTGTTGGTAATT 768
           |||  ||||  |  ||  ||||   ||    | ||   ||   |    ||  | |  ||  |
Db     316 ACACAAATTGGCCCACCAGAGGTGGGACTGACTACAGATGAGAAGTCCATTTCTGTTGTC 375

Qy     769 CTCCATGCTCCAAATTTACCATATAGATACCAAAAGGAAAAAAATGTATCTATAGAAGA 827
           ||    ||||||  |        | |||  |  |  |  ||      |||  ||  ||  || |
Db     376 CTGACAGCTCCAGAGAAGTGGAAGAGAAATCCAGAAGACCTTCCTGTTTCCATGCAACA 434


RESULT 8
US-08-943-087-15
; Sequence 15, Application US/08943087
; Patent No. 5945511
;  GENERAL INFORMATION:
;    APPLICANT:  Lok, Si
;    APPLICANT:  Kho, Choon J.
;    APPLICANT:  Jelmberg, Anna C.
;    APPLICANT:  Adams, Robyn L.
;    APPLICANT:  Whitmore, Theodore E.
;    APPLICANT:  Farrah, Theresa M.
;    TITLE OF INVENTION:  CYTOKINE RECEPTOR
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ZymoGenetics, Inc.
;      STREET:  1201 Eastlake Avenue East
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98102
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/943,087
;      FILING DATE:
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/803,305
;      FILING DATE:  20-FEB-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lunn, Paul G
;      REGISTRATION NUMBER:  32,743
;      REFERENCE/DOCKET NUMBER:  96-24C1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206-442-6627
;      TELEFAX:  206-442-6678
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1659 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  1...1659
;      OTHER INFORMATION:
US-08-943-087-15

  Query Match             5.1%;  Score 67;  DB 2;  Length 1659;
  Best Local Similarity   51.5%;  Pred. No. 1e-06;
  Matches  154;  Conservative    0;  Mismatches  145;  Indels    0;  Gaps    0;

Qy     529 AAATATGGACAGAGACAATGGAAAAATAAAGAAGACTGTTGGGGTACTCAAGAACTCTCT 588
           | |||||| || |   |||||  ||||||  ||| ||| |   ||   |   |  ||
Db     223 ATATATGGGCAAAAGAAATGGCTGAATAAATCAGAATGTAGAAATATCAATAGAACCTAC 282

Qy     589 TGTGACCTTACCAGTGAAACCTCAGACATACAGGAACCTTATTACGGGAGGGTGAGGGCG 648
           |||||  |||  |   ||||||  ||  ||      |  | |  |||||  |  |  || | |||
Db     283 TGTGATCTTTCTGCTGAAACTTCTGATTACGAACACCAGTATTATGCCAAAGTTAAGGCC 342

Qy     649 GCCTCGGCTGGGAGCTACTCAGAATGGAGCATGACGCCGCGGTTCACTCCCTGGTGGGAA 708
             | ||     |  |  ||  |||||      |     ||||||  |||  |  |  |||
Db     343 ATTTGGGGAACAAAGTGTTCCAAATGGGCTGAAAGTGGACGGTTCTATCCTTTTTTAGAA 402

Qy     709 ACAAAAATAGATCCTCCAGTCATGAATATAACCCAAGTCAATGGCTCTTTGTTGGTAATT 768
           |||  ||||  |  ||  ||||   ||    | ||   ||   |    ||  | |  ||  |
Db     403 ACACAAATTGGCCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTTCTGTTGTC 462

Qy     769 CTCCATGCTCCAAATTTACCATATAGATACCAAAAGGAAAAAAATGTATCTATAGAAGA 827
           ||    ||||||  |        | |||  |  |  |  ||      |||  ||  ||  || |
Db     463 CTGACAGCTCCAGAGAAGTGGAAGAGAAATCCAGAAGATCTTCCTGTTTCCATGCAACA 521


RESULT 9
US-08-943-087-17
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; Sequence 17, Application US/08943087
; Patent No. 5945511
;  GENERAL INFORMATION:
;    APPLICANT:  Lok, Si
;    APPLICANT:  Kho, Choon J.
;    APPLICANT:  Jelmberg, Anna C.
;    APPLICANT:  Adams, Robyn L.
;    APPLICANT:  Whitmore, Theodore E.
;    APPLICANT:  Farrah, Theresa M.
;    TITLE OF INVENTION:  CYTOKINE RECEPTOR
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ZymoGenetics, Inc.
;      STREET:  1201 Eastlake Avenue East
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98102
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/943,087
;      FILING DATE:
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/803,305
;      FILING DATE:  20-FEB-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lunn, Paul G
;      REGISTRATION NUMBER:  32,743
;      REFERENCE/DOCKET NUMBER:  96-24C1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206-442-6627
;      TELEFAX:  206-442-6678
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  17:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1659 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  1...1659
;      OTHER INFORMATION:
;US-08-943-087-17

  Query Match             5.1%;  Score 67;  DB 2;  Length 1659;
  Best Local Similarity   51.5%;  Pred. No. 1e-06;
  Matches  154;  Conservative    0;  Mismatches  145;  Indels    0;  Gaps    0;

Qy     529 AAATATGGACAGAGACAATGGAAAAATAAAGAAGACTGTTGGGGTACTCAAGAACTCTCT 588
           | |||||| || |   |||||   ||||||  ||| ||  |   ||   |   |  ||
Db     223 ATATATGGGCAAAAGAAATGGCTGAATAAATCAGAGTGCAGAAATATCAATAGAACCTAC 282

Qy     589 TGTGACCTTACCAGTGAAACCTCAGACATACAGGAACCTTATTACGGGAGGGTGAGGGCG 648
           |||||  |||  |   |||  ||  ||  ||     ||  |  |  |||||  |   |  ||  |  |||
Db     283 TGTGATCTTTCTGCTGAGACTTCTGATTACGAGCACCAGTATTATGCCAAAGTTAAGGCC 342

Qy     649 GCCTCGGCTGGGAGCTACTCAGAATGGAGCATGACGCCGCGGTTCACTCCCTGGTGGGAA 708
             | ||     |  |  ||  |||||     ||     ||||||  |||  |   |  ||
Db     343 ATTTGGGGAACAAAGTGTTCCAAATGGGCTGAGAGTGGACGGTTCTATCCTTTTTTAGAG 402

Qy     709 ACAAAAATAGATCCTCCAGTCATGAATATAACCCAAGTCAATGGCTCTTTGTTGGTAATT 768
           |||  ||||  |  ||  ||||   ||    | ||   ||   |    ||  |  |  ||  |
Db     403 ACACAAATTGGCCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTTCTGTTGTC 462

Qy     769 CTCCATGCTCCAAATTTACCATATAGATACCAAAAGGAAAAAAATGTATCTATAGAAGA 827
           ||    |||||| |        | |||  |  |  |  ||||      |||  ||  ||  ||  |
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Db     463 CTGACAGCTCCAGAGAAGTGGAAGAGAAATCCAGAGGATCTTCCTGTTTCCATGCAACA 521


RESULT 10
US-08-943-087-23
; Sequence 23, Application US/08943087
; Patent No. 5945511
;  GENERAL INFORMATION:
;    APPLICANT:  Lok, Si
;    APPLICANT:  Kho, Choon J.
;    APPLICANT:  Jelmberg, Anna C.
;    APPLICANT:  Adams, Robyn L.
;    APPLICANT:  Whitmore, Theodore E.
;    APPLICANT:  Farrah, Theresa M.
;    TITLE OF INVENTION:  CYTOKINE RECEPTOR
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ZymoGenetics, Inc.
;      STREET:  1201 Eastlake Avenue East
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98102
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/943,087
;      FILING DATE:
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/803,305
;      FILING DATE:  20-FEB-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lunn, Paul G
;      REGISTRATION NUMBER:  32,743
;      REFERENCE/DOCKET NUMBER:  96-24C1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206-442-6627
;      TELEFAX:  206-442-6678
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  23:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1659 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  1...1659
;      OTHER INFORMATION:
US-08-943-087-23

  Query Match             5.1%;  Score 67;  DB 2;  Length 1659;
  Best Local Similarity   51.5%;  Pred. No. 1e-06;
  Matches  154;  Conservative    0;  Mismatches  145;  Indels    0;  Gaps    0;

Qy     529 AAATATGGACAGAGACAATGGAAAAATAAAGAAGACTGTTGGGGTACTCAAGAACTCTCT 588
           | |||||| || |   |||||   ||||||  ||| ||  |   ||   |   |  ||
Db     223 ATATATGGGCAAAAGAAATGGCTGAATAAATCAGAATGCAGAAATATCAATAGAACCTAC 282

Qy     589 TGTGACCTTACCAGTGAAACCTCAGACATACAGGAACCTTATTACGGGAGGGTGAGGGCG 648
           |||||  |||  |   ||||||  ||  |||     |  |  |  |||||  |   |  ||  |  |||
Db     283 TGTGATCTTTCTGCTGAAACTTCTGACTACGAACATCAGTATTATGCCAAAGTTAAGGCC 342

Qy     649 GCCTCGGCTGGGAGCTACTCAGAATGGAGCATGACGCCGCGGTTCACTCCCTGGTGGGAA 708
             | ||     |  |  ||  |||||     |     ||||||  |||  |   |  |||
Db     343 ATTTGGGGCACAAAGTGTTCCAAATGGGCTGAAAGTGGCCGGTTCTATCCTTTTTTAGAA 402

Qy     709 ACAAAAATAGATCCTCCAGTCATGAATATAACCCAAGTCAATGGCTCTTTGTTGGTAATT 768
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Db    403 ACACAAATTGGCCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTTCTGTTGTC 462

Qy    769 CTCCATGCTCCAAATTTACCATATAGATACCAAAAGGAAAAAAATGTATCTATAGAAGA 827
Db    463 CTGACAGCTCCAGAGAAGTGGAAGAGAAATCCAGAAGACCTTCCTGTTTCCATGCAACA 521
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RESULT 11
US-08-943-087-1
; Sequence 1, Application US/08943087
; Patent No. 5945511
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Farrah, Theresa M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,087
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/803,305
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-24C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3516 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 237...1895
; OTHER INFORMATION:
US-08-943-087-1

Query Match 5.1%; Score 67; DB 2; Length 3516;
Best Local Similarity 51.5%; Pred. No. 1.3e-06;
Matches 154; Conservative 0; Mismatches 145; Indels 0; Gaps 0;

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Qy    529 AAATATGGACAGAGACAATGGAAAAATAAAGAAGACTGTTGGGGTACTCAAGAACTCTCT 588
Db    459 ATATATGGGCAAAAGAAATGGCTGAATAAATCAGAATGCAGAAATATCAATAGAACCTAC 518

Qy    589 TGTGACCTTACCAGTGAAACCTCAGACATACAGGAACCTTATTACGGGAGGGTGAGGGCG 648
Db    519 TGTGATCTTTCTGCTGAAACTTCTGACTACGAACACCAGTATTATGCCAAAGTTAAGGCC 578

Qy    649 GCCTCGGCTGGGAGCTACTCAGAATGGAGCATGACGCCGCGGTTCACTCCCTGGTGGGAA 708
Db    579 ATTTGGGGAACAAAGTGTTCCAAATGGGCTGAAAGTGGACGGTTCTATCCTTTTTTAGAA 638

Qy    709 ACAAAAATAGATCCTCCAGTCATGAATATAACCCAAGTCAATGGCTCTTTGTTGGTAATT 768
Db    639 ACACAAATTGGCCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTTCTGTTGTC 698

Qy    769 CTCCATGCTCCAAATTTACCATATAGATACCAAAAGGAAAAAAATGTATCTATAGAAGA 827
Db    699 CTGACAGCTCCAGAGAAGTGGAAGAGAAATCCAGAAGACCTTCCTGTTTCCATGCAACA 757
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RESULT 12
US-08-943-087-25
; Sequence 25, Application US/08943087
; Patent No. 5945511
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Farrah, Theresa M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,087
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/803,305
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-24C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1659 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...1659
; OTHER INFORMATION:
US-08-943-087-25

Query Match 5.1%; Score 66.8; DB 2; Length 1659;
Best Local Similarity 51.3%; Pred. No. 1.2e-06;
Matches 155; Conservative 0; Mismatches 147; Indels 0; Gaps 0;

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Qy    532 TATGGACAGAGACAATGGAAAAATAAAGAAGACTGTTGGGGTACTCAAGAACTCTCTTGT 591
Db    226 TATGGGCAAAAGAAATGGCTGAATAAATCAGAATGCAGAAATATCAATAGAACCTACTGT 285
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Qy     592 GACCTTACCAGTGAAACCTCAGACATACAGGAACCTTATTACGGGAGGGTGAGGGCGGCC 651
           || ||| |   |||||| || |||    |  | |  ||||| |  |  || | |||
Db     286 GATCTTTCTGCTGAAACTTCTGACTACGAACATCAGTATTATGCCAAAGTTAAGGCCATT 345

Qy     652 TCGGCTGGGAGCTACTCAGAATGGAGCATGACGCCGCGGTTCACTCCCTGGTGGGAAACA 711
           | ||     |  |  ||  |||||      |     ||||||  ||| |  |  ||||||
Db     346 TGGGGAACAAAGTGTTCCAAATGGGCTGAAAGTGGACGGTTCTATCCTTTTTTAGAAACA 405

Qy     712 AAAATAGATCCTCCAGTCATGAATATAACCCAAGTCAATGGCTCTTTGTTGGTAATTCTC 771
           ||||  |  || ||||   ||    | ||   ||   |    ||  | |  ||  | ||
Db     406 CAAATTGGCCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTTCTGTTGTCCTG 465

Qy     772 CATGCTCCAAATTTACCATATAGATACCAAAAGGAAAAAAATGTATCTATAGAAGATTAC 831
           ||||||  |      | |||  | | | | ||      ||| || ||  || |   |
Db     466 ACAGCTCCAGAGAAGTGGAAGAGAAATCCAGAAGACCTTCCTGTTTCCATGCAACAAATC 525

Qy     832 TA 833
           ||
Db     526 TA 527
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RESULT 13
US-08-943-087-21
; Sequence 21, Application US/08943087
; Patent No. 5945511
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Farrah, Theresa M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,087
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/803,305
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-24C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1659 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...1659
; OTHER INFORMATION:

US-08-943-087-21

Query Match 5.0%; Score 66.4; DB 2; Length 1659;
Best Local Similarity 51.3%; Pred. No. 1.4e-06;
Matches 154; Conservative 0; Mismatches 146; Indels 0; Gaps 0;

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Qy     528 TAAATATGGACAGAGACAATGGAAAAATAAAGAAGACTGTTGGGGTACTCAAGAACTCTC 587
           || |||||| || |   |||||   ||||||  ||| ||  |   ||   |   | ||
Db     222 TATATATGGGCAAAAGAAATGGCTGAATAAATCAGAATGCAGAAATATCAATAGAACCTA 281

Qy     588 TTGTGACCTTACCAGTGAAACCTCAGACATACAGGAACCTTATTACGGGAGGGTGAGGGC 647
           |||||| ||| |   ||||||  || |||    |  | |  ||||| |  |  || | |||
Db     282 CTGTGATCTTTCTGCTGAAACTTCTGACTACGAACACCAGTATTATGCCAAAGTTAAGGC 341

Qy     648 GGCCTCGGCTGGGAGCTACTCAGAATGGAGCATGACGCCGCGGTTCACTCCCTGGTGGGA 707
           | ||     |  |  ||  |||||      |     |||||  ||| |  |  ||
Db     342 CATTTGGGGCACAAAGTGTTCCAAATGGGCTGAAAGTGGCCGGTTTTATCCTTTTTTAGA 401

Qy     708 AACAAAAATAGATCCTCCAGTCATGAATATAACCCAAGTCAATGGCTCTTTGTTGGTAAT 767
           |||| |||| |  || ||||   ||    | ||   ||   |    ||  | |  ||  |
Db     402 AACACAAATTGGCCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTTCTGTTGT 461

Qy     768 TCTCCATGCTCCAAATTTACCATATAGATACCAAAAGGAAAAAAATGTATCTATAGAAGA 827
           ||    ||||||  |        | ||| | | | | ||      ||| || ||  || |
Db     462 CCTGACAGCTCCAGAGAAGTGGAAGAGAAATCCAGAAGACCTTCCTGTTTCCATGCAACA 521
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RESULT 14
US-08-943-087-57
; Sequence 57, Application US/08943087
; Patent No. 5945511
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Farrah, Theresa M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,087
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/803,305
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-24C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 663 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...663
; OTHER INFORMATION:
US-08-943-087-57

Query Match 5.0%; Score 65.4; DB 2; Length 663;
Best Local Similarity 51.2%; Pred. No. 1.9e-06;
Matches 153; Conservative 0; Mismatches 146; Indels 0; Gaps 0;

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Db     136 ATATATGGGCAAAAGAAATGGCTGAATAAATCAGACTGCAGAAATATCAATAGAACCTAC 195

Qy     589 TGTGACCTTACCAGTGAAACCTCAGACATACAGGAACCTTATTACGGGAGGGTGAGGGCG 648
           |||||  |||  |   |||  ||  ||  |||     |  | |  |||||  |  |  || | |||
Db     196 TGTGATCTTTCTGCTGACACTTCTGACTACGACCACCAGTATTATGCCAAAGTTAAGGCC 255

       649 GCCTCGGCTGGGAGCTACTCAGAATGGAGCATGACGCCGCGGTTCACTCCCTGGTGGGAA 708
           | ||     |  |  ||  |||||      |    ||||||  |||  |  |  ||
       256 ATTTGGGGAACAAAGTGTTCCAAATGGGCTGACAGTGGACGGTTCTATCCTTTTTTAGAC 315

Qy     709 ACAAAAATAGATCCTCCAGTCATGAATATAACCCAAGTCAATGGCTCTTTGTTGGTAATT 768
           |||  ||||  |  ||  ||||    ||    | ||   ||   |    ||  | |  ||  |
Db     316 ACACAAATTGGCCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTTCTGTTGTC 375

Qy     769 CTCCATGCTCCAAATTTACCATATAGATACCAAAAGGAAAAAAATGTATCTATAGAAGA 827
           ||    ||||||  |       | |||  |  |  |  |  ||     |||  ||  ||  || |
Db     376 CTGACAGCTCCAGAGAAGTGGAAGAGAAATCCAGACGACCTTCCTGTTTCCATGCAACA 434
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RESULT 15
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; Sequence 29, Application US/08943087
; Patent No. 5945511
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Farrah, Theresa M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,087
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/803,305
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-24C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 29:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 1659 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...1659
; OTHER INFORMATION:
US-08-943-087-29

Query Match 5.0%; Score 65.4; DB 2; Length 1659;
Best Local Similarity 51.2%; Pred. No. 2.5e-06;
Matches 153; Conservative 0; Mismatches 146; Indels 0; Gaps 0;

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Qy     529 AAATATGGACAGAGACAATGGAAAAATAAAGAAGACTGTTGGGGTACTCAAGAACTCTCT 588
           | |||||| || |   | |||   |||||   ||| ||  |   ||   |   |  ||
Db     223 ATATATGGGCAAAAGAAGTGGCTGAATAAGTCAGAATGCAGAAATATCAATAGAACCTAC 282

Qy     589 TGTGACCTTACCAGTGAAACCTCAGACATACAGGAACCTTATTACGGGAGGGTGAGGGCG 648
           |||||  |||  |   ||||||  ||  |||     |  | |  |||||  |  | |||  | |||
Db     283 TGTGATCTTTCTGCTGAAACTTCTGACTACGAACACCAGTATTATGCCAAGGTTAAGGCC 342

Qy     649 GCCTCGGCTGGGAGCTACTCAGAATGGAGCATGACGCCGCGGTTCACTCCCTGGTGGGAA 708
           | ||     |  |  ||  | |||      |     ||||||  |||  |  | ||||
Db     343 ATTTGGGGAACAAAGTGTTCCAAGTGGGCTGAAAGTGGACGGTTCTATCCTTTTTTGGAA 402

Qy     709 ACAAAAATAGATCCTCCAGTCATGAATATAACCCAAGTCAATGGCTCTTTGTTGGTAATT 768
           |||  ||||  |  ||  ||||    ||    | ||   ||   |    ||  | |  ||  |
Db     403 ACACAAATTGGCCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTTCTGTTGTC 462

Qy     769 CTCCATGCTCCAAATTTACCATATAGATACCAAAAGGAAAAAAATGTATCTATAGAAGA 827
           ||    ||||||  |       | |||  |  |  |  |  ||     |||  ||  ||  || |
Db     463 CTGACAGCTCCAGAGAAGTGGAAGAGAAATCCAGAAGACCTTCCTGTTTCCATGCAACA 521
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Search completed: December 22, 2002, 09:12:33
Job time : 65 secs

GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: December 22, 2002, 08:38:11 ; Search time 63 Seconds
(without alignments)
8302.512 Million cell updates/sec

Title: US-09-964-994-1
Perfect score: 1318
Sequence: 1 cagtttcttcatctgtaaca.....aaaaaaaaaaaaaaaaaaaa 1318

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 356696 seqs, 198428768 residues

Total number of hits satisfying chosen parameters: 713392

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
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2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
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7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
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11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1318	100.0	1318	10	US-09-964-994-1	Sequence 1, Appli
	2	831.6	63.1	2149	10	US-09-728-911-1	Sequence 1, Appli
	3	398.2	30.2	693	10	US-09-728-911-3	Sequence 3, Appli
c	4	171.4	13.0	478	10	US-09-864-761-15058	Sequence 15058, A
	5	171.4	13.0	528	10	US-09-864-761-6687	Sequence 6687, Ap
	6	170	12.9	170	10	US-09-864-761-23421	Sequence 23421, A
c	7	128	9.7	128	10	US-09-864-761-31588	Sequence 31588, A
	8	75.4	5.7	1806	10	US-09-746-359A-36	Sequence 36, Appl
c	9	69.2	5.3	424	10	US-09-960-352-11218	Sequence 11218, A
	10	67	5.1	1720	10	US-09-746-359A-52	Sequence 52, Appl
	11	67	5.1	1750	12	US-10-052-586-397	Sequence 397, App
	12	67	5.1	1801	10	US-09-746-359A-22	Sequence 22, Appl
	13	67	5.1	3516	10	US-09-746-359A-10	Sequence 10, Appl
c	14	66.2	5.0	277	10	US-09-960-352-12673	Sequence 12673, A
c	15	64.2	4.9	375	10	US-09-960-352-15014	Sequence 15014, A
c	16	63	4.8	447	10	US-09-960-352-8533	Sequence 8533, Ap
c	17	62.2	4.7	308	10	US-09-960-352-7670	Sequence 7670, Ap
	18	61.4	4.7	277	10	US-09-960-352-12673	Sequence 12673, A
	19	61.4	4.7	1492	10	US-09-925-299-112	Sequence 112, App
c	20	60.8	4.6	300	10	US-09-960-352-6251	Sequence 6251, Ap
	21	60.4	4.6	3772	9	US-09-992-598-61	Sequence 61, Appl
	22	60.4	4.6	3772	9	US-09-989-293A-61	Sequence 61, Appl
	23	60.4	4.6	3772	10	US-09-989-722-61	Sequence 61, Appl
	24	60.4	4.6	3772	10	US-09-989-723-61	Sequence 61, Appl
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	26	60.4	4.6	3772	10	US-09-989-727-61	Sequence 61, Appl
	27	60.4	4.6	3772	10	US-09-989-731-61	Sequence 61, Appl
	28	60.4	4.6	3772	10	US-09-989-732-61	Sequence 61, Appl
	29	60.4	4.6	3772	10	US-09-991-073-61	Sequence 61, Appl
	30	60.4	4.6	3772	10	US-09-990-442-61	Sequence 61, Appl
	31	60.4	4.6	3772	10	US-09-991-163-61	Sequence 61, Appl
	32	60.4	4.6	3772	10	US-09-993-604-61	Sequence 61, Appl
	33	60.4	4.6	3772	10	US-09-990-456-61	Sequence 61, Appl
	34	60.4	4.6	3772	10	US-09-989-721-61	Sequence 61, Appl
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c	36	60.2	4.6	415	10	US-09-960-352-6869	Sequence 6869, Ap
c	37	59.6	4.5	239	10	US-09-960-352-11438	Sequence 11438, A
	38	59.6	4.5	312	10	US-09-960-352-8414	Sequence 8414, Ap
c	39	59	4.5	347	10	US-09-960-352-3371	Sequence 3371, Ap
	40	58.8	4.5	302	10	US-09-925-299-710	Sequence 710, App
c	41	58.6	4.4	419	10	US-09-960-352-11234	Sequence 11234, A
c	42	58.4	4.4	236	10	US-09-960-352-12183	Sequence 12183, A
c	43	58.4	4.4	298	10	US-09-960-352-1004	Sequence 1004, Ap
	44	58.2	4.4	325	10	US-09-764-846-30	Sequence 30, Appl
	45	58.2	4.4	621	10	US-09-764-846-105	Sequence 105, App

ALIGNMENTS

RESULT 1
US-09-964-994-1
; Sequence 1, Application US/09964994
; Patent No. US20020137909A1
; GENERAL INFORMATION:
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; TITLE OF INVENTION: NOVEL POLYPEPTIDES HAVING SEQUENCE SIMILARITY TO
; TITLE OF INVENTION: CYTOKINE RECEPTORS AND NUCLEIC ACIDS ENCODING THE SAME
; FILE REFERENCE: P3121R1
; CURRENT APPLICATION NUMBER: US/09/964,994
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 60/191,015
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 09/941,992
; PRIOR FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 7
; SEQ ID NO 1
; LENGTH: 1318
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-964-994-1

Query Match 100.0%; Score 1318; DB 10; Length 1318;
Best Local Similarity 100.0%; Pred. No. 6.5e-254;
Matches 1318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 CAGTTTCTTCATCTGTAACATCAAATGAATAATAATACCAATCTCCTAGACTTCATAAGA 60
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Db       1 CAGTTTCTTCATCTGTAACATCAAATGAATAATAATACCAATCTCCTAGACTTCATAAGA 60

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Qy    181 TTGGTCCTGAGCTGGTTAAAAGGAACACTGGTTGCCTGAACAGTCACACTTGCAACCATG 240
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Db    181 TTGGTCCTGAGCTGGTTAAAAGGAACACTGGTTGCCTGAACAGTCACACTTGCAACCATG 240

Qy    241 ATGCCTAAACATTGCTTTCTAGGCTTCCTCATCAGTTTCTTCCTTACTGGTGTAGCAGGA 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 ATGCCTAAACATTGCTTTCTAGGCTTCCTCATCAGTTTCTTCCTTACTGGTGTAGCAGGA 300

Qy    301 ACTCAGTCAACGCATGAGTCTCTGAAGCCTCAGAGGGTACAATTTCAGTCCCGAAATTTT 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 ACTCAGTCAACGCATGAGTCTCTGAAGCCTCAGAGGGTACAATTTCAGTCCCGAAATTTT 360

Qy    361 CACAACATTTTGCAATGGCAGCCTGGGAGGGCACTTACTGGCAACAGCAGTGTCTATTTT 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 CACAACATTTTGCAATGGCAGCCTGGGAGGGCACTTACTGGCAACAGCAGTGTCTATTTT 420

Qy    421 GTGCAGTACAAAATCATGTTCTCATGCAGCATGAAAAGCTCTCACCAGAAGCCAAGTGGA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GTGCAGTACAAAATCATGTTCTCATGCAGCATGAAAAGCTCTCACCAGAAGCCAAGTGGA 480

Qy    481 TGCTGGCAGCACATTTCTTGTAACTTCCCAGGCTGCAGAACATTGGCTAAATATGGACAG 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 TGCTGGCAGCACATTTCTTGTAACTTCCCAGGCTGCAGAACATTGGCTAAATATGGACAG 540

Qy    541 AGACAATGGAAAAATAAAGAAGACTGTTGGGGTACTCAAGAACTCTCTTGTGACCTTACC 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 AGACAATGGAAAAATAAAGAAGACTGTTGGGGTACTCAAGAACTCTCTTGTGACCTTACC 600

Qy    601 AGTGAAACCTCAGACATACAGGAACCTTATTACGGGAGGGTGAGGGCGGCCTCGGCTGGG 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 AGTGAAACCTCAGACATACAGGAACCTTATTACGGGAGGGTGAGGGCGGCCTCGGCTGGG 660

Qy    661 AGCTACTCAGAATGGAGCATGACGCCGCGGTTCACTCCCTGGTGGGAAACAAAAATAGAT 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 AGCTACTCAGAATGGAGCATGACGCCGCGGTTCACTCCCTGGTGGGAAACAAAAATAGAT 720

Qy    721 CCTCCAGTCATGAATATAACCCAAGTCAATGGCTCTTTGTTGGTAATTCTCCATGCTCCA 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 CCTCCAGTCATGAATATAACCCAAGTCAATGGCTCTTTGTTGGTAATTCTCCATGCTCCA 780

Qy    781 AATTTACCATATAGATACCAAAAGGAAAAAAATGTATCTATAGAAGATTACTATGAACTA 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 AATTTACCATATAGATACCAAAAGGAAAAAAATGTATCTATAGAAGATTACTATGAACTA 840

Qy    841 CTATACCGAGTTTTTATAATTAACAATTCACTAGAAAAGGAGCAAAAGGTTTATGAAGGG 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 CTATACCGAGTTTTTATAATTAACAATTCACTAGAAAAGGAGCAAAAGGTTTATGAAGGG 900

Qy    901 GCTCACAGAGCGGTTGAAATTGAAGCTCTAACACCACACTCCAGCTACTGTGTAGTGGCT 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 GCTCACAGAGCGGTTGAAATTGAAGCTCTAACACCACACTCCAGCTACTGTGTAGTGGCT 960

Qy    961 GAAATATATCAGCCCATGTTAGACAGAAGAAGTCAGAGAAGTGAAGAGAGATGTGTGGAA 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 GAAATATATCAGCCCATGTTAGACAGAAGAAGTCAGAGAAGTGAAGAGAGATGTGTGGAA 1020

Qy   1021 ATTCCATGACTTGTGGAATTTGGCATTCAGCAATGTGGAAATTCTAAAGCTCCCTGAGAA 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 ATTCCATGACTTGTGGAATTTGGCATTCAGCAATGTGGAAATTCTAAAGCTCCCTGAGAA 1080

Qy   1081 CAGGATGACTCGTGTTTGAAGGATCTTATTTAAAATTGTTTTTGTATTTTCTTAAAGCAA 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 CAGGATGACTCGTGTTTGAAGGATCTTATTTAAAATTGTTTTTGTATTTTCTTAAAGCAA 1140

Qy   1141 TATTCACTGTTACACCTTGGGGACTTCTTTGTTTATCCATTCTTTTATCCTTTATATTTC 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 TATTCACTGTTACACCTTGGGGACTTCTTTGTTTATCCATTCTTTTATCCTTTATATTTC 1200

Qy   1201 ATTTGTAAACTATATTTGAACGACATTCCCCCCGAAAAATTGAAATGTAAAGATGAGGCA 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 ATTTGTAAACTATATTTGAACGACATTCCCCCCGAAAAATTGAAATGTAAAGATGAGGCA 1260

Qy   1261 GAGAATAAAGTGTTCTATGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1318
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 GAGAATAAAGTGTTCTATGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1318
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RESULT 2
US-09-728-911-1
; Sequence 1, Application US/09728911
; Patent No. US20020012669A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Kindsvogel, Wayne
; APPLICANT: Chen, Zhi
; TITLE OF INVENTION: Human Cytokine Receptor
; FILE REFERENCE: 99-93
; CURRENT APPLICATION NUMBER: US/09/728,911
; CURRENT FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 60/169,049
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: US 60/232,219
; PRIOR FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: US 60/244,610
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 2149
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(693)
US-09-728-911-1

Query Match 63.1%; Score 831.6; DB 10; Length 2149;
Best Local Similarity 90.4%; Pred. No. 5.8e-157;
Matches 951; Conservative 0; Mismatches 4; Indels 97; Gaps 2;

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Qy    238 ATGATGCCTAAACATTGCTTTCTAGGCTTCCTCATCAGTTTCTTCCTTACTGGTGTAGCA 297
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGATGCCTAAACATTGCTTTCTAGGCTTCCTCATCAGTTTCTTCCTTACTGGTGTAGCA 60

Qy    298 GGAACTCAGTCAACGCATGAGTCTCTGAAGCCTCAGAGGGTACAATTTCAGTCCCGAAAT 357
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GGAACTCAGTCAACGCATGAGTCTCTGAAGCCTCAGAGGGTACAATTTCAGTCCCGAAAT 120

Qy    358 TTTCACAACATTTTGCAATGGCAGCCTGGGAGGGCACTTACTGGCAACAGCAGTGTCTAT 417
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 TTTCACAACATTTTGCAATGGCAGCCTGGGAGGGCACTTACTGGCAACAGCAGTGTCTAT 180

Qy    418 TTTGTGCAGTACAAAATCATGTTCTCATGCAGCATGAAAAGCTCTCACCAGAAGCCAAGT 477
          |||||||||||||||||
Db    181 TTTGTGCAGTACAAAAT---------------------------------------------- 197

Qy    478 GGATGCTGGCAGCACATTTCTTGTAACTTCCCAGGCTGCAGAACATTGGCTAAATATGGA 537
                                                                |||||||
Db    198 ----------------------------------------------------ATATGGA 204

Qy    538 CAGAGACAATGGAAAAATAAAGAAGACTGTTGGGGTACTCAAGAACTCTCTTGTGACCTT 597
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    205 CAGAGACAATGGAAAAATAAAGAAGACTGTTGGGGTACTCAAGAACTCTCTTGTGACCTT 264

Qy    598 ACCAGTGAAACCTCAGACATACAGGAACCTTATTACGGGAGGGTGAGGGCGGCCTCGGCT 657
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    265 ACCAGTGAAACCTCAGACATACAGGAACCTTATTACGGGAGGGTGAGGGCGGCCTCGGCT 324

Qy    658 GGGAGCTACTCAGAATGGAGCATGACGCCGCGGTTCACTCCCTGGTGGGAAACAAAAATA 717
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    325 GGGAGCTACTCAGAATGGAGCATGACGCCGCGGTTCACTCCCTGGTGGGAAACAAAAATA 384
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Qy    718 GATCCTCCAGTCATGAATATAACCCAAGTCAATGGCTCTTTGTTGGTAATTCTCCATGCT 777
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    385 GATCCTCCAGTCATGAATATAACCCAAGTCAATGGCTCTTTGTTGGTAATTCTCCATGCT 444

Qy    778 CCAAATTTACCATATAGATACCAAAAGGAAAAAAATGTATCTATAGAAGATTACTATGAA 837
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    445 CCAAATTTACCATATAGATACCAAAAGGAAAAAAATGTATCTATAGAAGATTACTATGAA 504

Qy    838 CTACTATACCGAGTTTTTATAATTAACAATTCACTAGAAAAGGAGCAAAAGGTTTATGAA 897
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    505 CTACTATACCGAGTTTTTATAATTAACAATTCACTAGAAAAGGAGCAAAAGGTTTATGAA 564

Qy    898 GGGGCTCACAGAGCGGTTGAAATTGAAGCTCTAACACCACACTCCAGCTACTGTGTAGTG 957
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    565 GGGGCTCACAGAGCGGTTGAAATTGAAGCTCTAACACCACACTCCAGCTACTGTGTAGTG 624

Qy    958 GCTGAAATATATCAGCCCATGTTAGACAGAAGAAGTCAGAGAAGTGAAGAGAGATGTGTG 1017
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    625 GCTGAAATATATCAGCCCATGTTAGACAGAAGAAGTCAGAGAAGTGAAGAGAGATGTGTG 684

      1018 GAAATTCCATGACTTGTGGAATTTGGCATTCAGCAATGTGGAAATTCTAAAGCTCCCTGA 1077
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    685 GAAATTCCATGACTTGTGGAATTTGGCATTCAGCAATGTGGAAATTCTAAAGCTCCCTGA 744

Qy   1078 GAACAGGATGACTCGTGTTTGAAGGATCTTATTTAAAATTGTTTTTGTATTTTCTTAAAG 1137
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    745 GAACAGGATGACTCGTGTTTGAAGGATCTTATTTAAAATTGTTTTTGTATTTTCTTAAAG 804

Qy   1138 CAATATTCACTGTTACACCTTGGGGACTTCTTTGTTTATCCATTCTTTTATCCTTTATAT 1197
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    805 CAATATTCACTGTTACACCTTGGGGACTTCTTTGTTTATCCATTCTTTTATCCTTTATAT 864

Qy   1198 TTCATTTGTAAACTATATTTGAACGACATTCCCCCCGAAAAATTGAAATGTAAAGATGAG 1257
          ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    865 TTCATTT-TAAACTATATTTGAACGACATTCCCCCCGAAAAATTGAAATGTAAAGATGAG 923

Qy   1258 GCAGAGAATAAAGTGTTCTATGAAAAAAAAAA 1289
          ||||||||||||||||||||||||||  | ||
Db    924 GCAGAGAATAAAGTGTTCTATGAAATTCAGAA 955
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RESULT 3
US-09-728-911-3
; Sequence 3, Application US/09728911
; Patent No. US20020012669A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Kindsvogel, Wayne
; APPLICANT: Chen, Zhi
; TITLE OF INVENTION: Human Cytokine Receptor
; FILE REFERENCE: 99-93
; CURRENT APPLICATION NUMBER: US/09/728,911
; CURRENT FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 60/169,049
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: US 60/232,219
; PRIOR FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: US 60/244,610
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 693
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: This degenerate nucleotide sequence encodes the
; OTHER INFORMATION: amino acid sequence of SEQ ID NO:2.
; NAME/KEY: misc_feature
; LOCATION: (1)...(693)
; OTHER INFORMATION: n = A,T,C or G

US-09-728-911-3

Query Match 30.2%; Score 398.2; DB 10; Length 693;
Best Local Similarity 51.0%; Pred. No. 9e-71;
Matches 402; Conservative 179; Mismatches 111; Indels 96; Gaps 1;

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Qy    238 ATGATGCCTAAACATTGCTTTCTAGGCTTCCTCATCAGTTTCTTCCTTACTGGTGTAGCA 297
          |||||||| ||:||:||:||::| || ||::| ||::: ||:|||::| || || || ||
Db      1 ATGATGCCNAARCAYTGYTTYYTNGGNTTYYTNATHWSNTTYTTYYTNACNGGNGTNGCN 60

Qy    298 GGAACTCAGTCAACGCATGAGTCTCTGAAGCCTCAGAGGGTACAATTTCAGTCCCGAAAT 357
          || || ||::: || ||:||::: :| ||::|| ||::| || ||:||:||::: :| ||:
Db     61 GGNACNCARWSNACNCAYGARWSNYTNAARCCNCARMGNGTNCARTTYCARWSNMGNAAY 120

Qy    358 TTTCACAACATTTTGCAATGGCAGCCTGGGAGGGCACTTACTGGCAACAGCAGTGTCTAT 417
          ||:||:||:||::| ||:|||||:|| || :| || :| || || ||::: :: || ||:
Db    121 TTYCAYAAYATHYTNCARTGGCARCCNGGNMGNGCNYTNACNGGNAAYWSNWSNGTNTAY 180

Qy    418 TTTGTGCAGTACAAAATCATGTTCTCATGCAGCATGAAAAGCTCTCACCAGAAGCCAAGT 477
          ||:|| ||:||:||:||
Db    181 TTYGTNCARTAYAARAT---------------------------------------------- 197

Qy    478 GGATGCTGGCAGCACATTTCTTGTAACTTCCCAGGCTGCAGAACATTGGCTAAATATGGA 537
                                                          :||:||
Db    198 ----------------------------------------------------HTAYGGN 204

Qy    538 CAGAGACAATGGAAAAATAAAGAAGACTGTTGGGGTACTCAAGAACTCTCTTGTGACCTT 597
          ||::| ||:|||||:||:||:||:||:||||| || ||:||::| :: ||:||::|
Db    205 CARMGNCARTGGAARAAYAARGARGAYTGYTGGGGNACNCARGARYTNWSNTGYGAYYTN 264

Qy    598 ACCAGTGAAACCTCAGACATACAGGAACCTTATTACGGGAGGGTGAGGGCGGCCTCGGCT 657
          || :: ||:|| :: ||:||:||:||:|| ||:||:|| :| || :| || || :: ||
Db    265 ACNWSNGARACNWSNGAYATHCARGARCCNTAYTAYGGNMGNGTNMGNGCNGCNWSNGCN 324

Qy    658 GGGAGCTACTCAGAATGGAGCATGACGCCGCGGTTCACTCCCTGGTGGGAAACAAAAATA 717
          || :: ||::: ||:|||:: ||||| || :| ||:|| || ||||||||:|| ||:||:
Db    325 GGNWSNTAYWSNGARTGGWSNATGACNCCNMGNTTYACNCCNTGGTGGGARACNAARATH 384

Qy    718 GATCCTCCAGTCATGAATATAACCCAAGTCAATGGCTCTTTGTTGGTAATTCTCCATGCT 777
          ||:|| || || |||||:||:|| ||:|| ||:|| :: :| :| || ||::| ||:||
Db    385 GAYCCNCCNGTNATGAAYATHACNCARGTNAAYGGNWSNYTNYTNGTNATHYTNCAYGCN 444

Qy    778 CCAAATTTACCATATAGATACCAAAAGGAAAAAAATGTATCTATAGAAGATTACTATGAA 837
          || ||::| || ||::| ||:||:||:||:||:||:|| :: ||:||:||:||:||:||:
Db    445 CCNAAYYTNCCNTAYMGNTAYCARAARGARAARAAYGTNWSNATHGARGAYTAYTAYGAR 504

Qy    838 CTACTATACCGAGTTTTTATAATTAACAATTCACTAGAAAAGGAGCAAAAGGTTTATGAA 897
          :| :| ||::| || ||:||:||:||:||::: :| ||:||:||:||:||:|| ||:||:
Db    505 YTNYTNTAYMGNGTNTTYATHATHAAYAAYWSNYTNGARAARGARCARAARGTNTAYGAR 564

Qy    898 GGGGCTCACAGAGCGGTTGAAATTGAAGCTCTAACACCACACTCCAGCTACTGTGTAGTG 957
          || || ||::| || || ||:||:||:|| :| || || ||::: :: ||:||:|| ||
Db    565 GGNGCNCAYMGNGCNGTNGARATHGARGCNYTNACNCCNCAYWSNWSNTAYTGYGTNGTN 624

Qy    958 GCTGAAATATATCAGCCCATGTTAGACAGAAGAAGTCAGAGAAGTGAAGAGAGATGTGTG 1017
          || ||:||:||:||:|| |||:| ||::| :| :: ||::| :: ||:||::| ||:||
Db    625 GCNGARATHTAYCARCCNATGYTNGAYMGNMGNWSNCARMGNWSNGARGARMGNTGYGTN 684

Qy   1018 GAAATTCC 1025
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Db    685 GARATHCC 692
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RESULT 4
US-09-864-761-15058/c
; Sequence 15058, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO

; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 15058
; LENGTH: 478
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL050337.6
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.67
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.77
US-09-864-761-15058

Query Match 13.0%; Score 171.4; DB 10; Length 478;
Best Local Similarity 99.4%; Pred. No. 1.2e-25;
Matches 172; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy    708 AACAAAAATAGATCCTCCAGTCATGAATATAACCCAAGTCAATGGCTCTTTGTTGGTAAT 767
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Db    475 AGCAAAAATAGATCCTCCAGTCATGAATATAACCCAAGTCAATGGCTCTTTGTTGGTAAT 416

Qy    768 TCTCCATGCTCCAAATTTACCATATAGATACCAAAAGGAAAAAAATGTATCTATAGAAGA 827
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    415 TCTCCATGCTCCAAATTTACCATATAGATACCAAAAGGAAAAAAATGTATCTATAGAAGA 356

Qy    828 TTACTATGAACTACTATACCGAGTTTTTATAATTAACAATTCACTAGAAAAGG 880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    355 TTACTATGAACTACTATACCGAGTTTTTATAATTAACAATTCACTAGAAAAGG 303
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RESULT 5
US-09-864-761-6687
; Sequence 6687, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 6687
; LENGTH: 528
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL158138.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.5
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.8
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.5
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.3
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.9
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.7
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.3
US-09-864-761-6687

Query Match 13.0%; Score 171.4; DB 10; Length 528;
Best Local Similarity 99.4%; Pred. No. 1.3e-25;
Matches 172; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy    708 AACAAAAATAGATCCTCCAGTCATGAATATAACCCAAGTCAATGGCTCTTTGTTGGTAAT 767
          | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    176 AGCAAAAATAGATCCTCCAGTCATGAATATAACCCAAGTCAATGGCTCTTTGTTGGTAAT 235

Qy    768 TCTCCATGCTCCAAATTTACCATATAGATACCAAAAGGAAAAAAATGTATCTATAGAAGA 827
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     236 TCTCCATGCTCCAAATTTACCATATAGATACCAAAAGGAAAAAAATGTATCTATAGAAGA 295

Qy     828 TTACTATGAACTACTATACCGAGTTTTTATAATTAACAATTCACTAGAAAAGG 880
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     296 TTACTATGAACTACTATACCGAGTTTTTATAATTAACAATTCACTAGAAAAGG 348


RESULT 6
US-09-864-761-23421
; Sequence 23421, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  APPLICANT:  Chen, Wensheng
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
;  TITLE OF INVENTION:  GENE EXPRESSION ANALYSIS BY MICROARRAY
;  FILE REFERENCE: Aeomica-X-1
;  CURRENT APPLICATION NUMBER: US/09/864,761
;  CURRENT FILING DATE:  2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/180,312
;  PRIOR FILING DATE: 2000-02-04
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 09/632,366
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 09/608,408
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: US 09/774,203
;  PRIOR FILING DATE: 2001-01-29
;  NUMBER OF SEQ ID NOS: 49117
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 23421
;    LENGTH: 170
;    TYPE: DNA
;    ORGANISM: Homo sapiens
;    FEATURE:
;    OTHER INFORMATION: MAP TO AL158138.1
;    OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.5
;    OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.8
;    OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.7
;    OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.5
;    OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.3
;    OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.9
;    OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.7
;    OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.3
;    OTHER INFORMATION: EST_HUMAN HIT: AV714177.1, EVALUE 2.00e-78
;    OTHER INFORMATION: SWISSPROT HIT: O28438, EVALUE 1.30e+00
US-09-864-761-23421

  Query Match             12.9%;  Score 170;  DB 10;  Length 170;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-25;
  Matches  170;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     710 CAAAAATAGATCCTCCAGTCATGAATATAACCCAAGTCAATGGCTCTTTGTTGGTAATTC 769
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 CAAAAATAGATCCTCCAGTCATGAATATAACCCAAGTCAATGGCTCTTTGTTGGTAATTC 60

Qy     770 TCCATGCTCCAAATTTACCATATAGATACCAAAAGGAAAAAAATGTATCTATAGAAGATT 829
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 TCCATGCTCCAAATTTACCATATAGATACCAAAAGGAAAAAAATGTATCTATAGAAGATT 120

Qy     830 ACTATGAACTACTATACCGAGTTTTTATAATTAACAATTCACTAGAAAAG 879
           |||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 ACTATGAACTACTATACCGAGTTTTTATAATTAACAATTCACTAGAAAAG 170


RESULT 7
US-09-864-761-31588/c
; Sequence 31588, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  APPLICANT:  Chen, Wensheng
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
;  TITLE OF INVENTION:  GENE EXPRESSION ANALYSIS BY MICROARRAY
;  FILE REFERENCE: Aeomica-X-1
;  CURRENT APPLICATION NUMBER: US/09/864,761
;  CURRENT FILING DATE:  2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/180,312
;  PRIOR FILING DATE: 2000-02-04
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 09/632,366
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 09/608,408
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: US 09/774,203
;  PRIOR FILING DATE: 2001-01-29
;  NUMBER OF SEQ ID NOS: 49117
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;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 31588
;   LENGTH: 128
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO AL050337.6
;   OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.67
;   OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.77
;   OTHER INFORMATION: EST_HUMAN HIT: AV714177.1, EVALUE 1.00e-53
;   OTHER INFORMATION: SWISSPROT HIT: O28438, EVALUE 1.80e+00
US-09-864-761-31588

  Query Match             9.7%;  Score 128;  DB 10;  Length 128;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-17;
  Matches  128;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     710 CAAAAATAGATCCTCCAGTCATGAATATAACCCAAGTCAATGGCTCTTTGTTGGTAATTC 769
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     128 CAAAAATAGATCCTCCAGTCATGAATATAACCCAAGTCAATGGCTCTTTGTTGGTAATTC 69

Qy     770 TCCATGCTCCAAATTTACCATATAGATACCAAAAGGAAAAAAATGTATCTATAGAAGATT 829
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      68 TCCATGCTCCAAATTTACCATATAGATACCAAAAGGAAAAAAATGTATCTATAGAAGATT 9

Qy     830 ACTATGAA 837
           ||||||||
Db       8 ACTATGAA 1


RESULT 8
US-09-746-359A-36
; Sequence 36, Application US/09746359A
; Patent No. US20020042366A1
; GENERAL INFORMATION:
;  APPLICANT: Thompson, Penny
;  APPLICANT:  Foster, Donald C.
;  APPLICANT:  Xu, Wenfeng
;  APPLICANT:  Madden, Karen L.
;  APPLICANT:  Kelly, James D.
;  APPLICANT:  Sprecher, Cindy A.
;  APPLICANT:  Blumberg, Hal
;  APPLICANT:  Eagan, Maribeth A.
;  APPLICANT:  Jaspers, Stephen R.
;  APPLICANT:  Chandrasekher, Yasmin A.
;  APPLICANT:  No. US20020042366A1ak, Julia E.
;  TITLE OF INVENTION: Method for Treating Inflammation
;  FILE REFERENCE: 99-108
;  CURRENT APPLICATION NUMBER: US/09/746,359A
;  CURRENT FILING DATE:  2001-05-21
;  PRIOR APPLICATION NUMBER: 60/171,969
;  PRIOR FILING DATE: 1999-12-23
;  PRIOR APPLICATION NUMBER: 60/213,341
;  PRIOR FILING DATE: 2000-06-22
;  NUMBER OF SEQ ID NOS: 72
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 36
;   LENGTH: 1806
;   TYPE: DNA
;   ORGANISM: Mus musculus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (38)...(1675)
US-09-746-359A-36

  Query Match             5.7%;  Score 75.4;  DB 10;  Length 1806;
  Best Local Similarity   48.1%;  Pred. No. 2.4e-06;
  Matches  214;  Conservative    0;  Mismatches  231;  Indels    0;  Gaps    0;

Qy     383 CTGGGAGGGCACTTACTGGCAACAGCAGTGTCTATTTTGTGCAGTACAAAATCATGTTCT 442
           | ||  | ||| || || |   |  | |||  |    |    |     || ||||  ||||
Db     123 CGGGACGCGCAGTTCCTTGTGTCTTCTGTGGTTTGCCTAAACCTACAAATATCACCTTCT 182

Qy     443 CATGCAGCATGAAAAGCTCTCACCAGAAGCCAAGTGGATGCTGGCAGCACATTTCTTGTA 502
           || || ||  |  |    |  || | |    | |  |     |  |          |
Db     183 TATCCATCAACATGAAGAATGTCCTGCATTGGAATCCACCAGAGAGTCTACACGGAGTTG 242

Qy     503 ACTTCCCAGGCTGCAGAACATTGGCTAAATATGGACAGAGACAATGGAAAAATAAAGAAG 562
           |  || ||  |         ||     | |||||| ||||   |||||   |||
Db     243 AAGTCACATACACTGTGCAATATTTCATATATGGGCAGAAGAAATGGCTGAATGCCTCTA 302

Qy     563 ACTGTTGGGGTACTCAAGAACTCTCTTGTGACCTTACCAGTGAAACCTCAGACATACAGG 622
           | ||  || |||   |       ||  |||||||||  |   ||| |||||||||    |
Db     303 AATGCGGGAGTATCAACAGGACCTACTGTGACCTTTCTGTTGAGACCTCAGACTATGAAC 362

Qy     623 AACCTTATTACGGGAGGGTGAGGGCGGCCTCGGCTGGGAGCTACTCAGAATGGAGCATGA 682
           | |  |  || |  |  |||| |||    | ||  |  || | ||| ||||||  |  ||
Db     363 ACCAGTTCTATGCCAAAGTGAAGGCCATTTGGGAAGCCAGGTGCTCCGAATGGGCCGAGA 422

Qy     683 CGCCGCGGTTCACTCCCTGGTGGGAAACAAAAATAGATCCTCCAGTCATGAATATAACCC 742
           ||   || |||  ||| |  | ||||||  || |    || ||||  ||     | ||
Db     423 CGGAACGCTTCTATCCTTTCTTGGAAACTCAAGTCAGCCCACCAGAGATTGCCCTGACAA 482

Qy     743 AAGTCAATGGCTCTTTGTTGGTAATTCTCCATGCTCCAAATTTACCATATAGATACCAAA 802
           | | |    ||  | |   |    ||    || ||| |         | ||| | | |
Db     483 CTGGCGAGAAGTCCATCTCTATTGCCCTGACAGCACCAGAGAAGTGGAAAAGAAATCCAC 542

Qy     803 AGGAAAAAAAATGTATCTATAGAAGA 827
           | ||  | | |||  |||||  || |
Db     543 AAGACCACACTGTTTCTATGCAACA 567


RESULT 9
US-09-960-352-11218/c
; Sequence 11218, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
;  APPLICANT: Warren, Wesley C.
;  APPLICANT:  Tao, Nengbing
;  APPLICANT:  Byatt, John C.
;  APPLICANT:  Mathialagan, Nagappan
;  TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
;  TITLE OF INVENTION:  MUSCLE AND FAT DEPOSITION
;  FILE REFERENCE: 16511.006/37-21(10298)C
;  CURRENT APPLICATION NUMBER: US/09/960,352
;  CURRENT FILING DATE:  2001-09-24
;  NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 11218
;   LENGTH: 424
;   TYPE: DNA
;   ORGANISM: Bos taurus
;   OTHER INFORMATION: Clone ID: 48-LIB3058-026-Q1-K1-D12
US-09-960-352-11218

  Query Match             5.3%;  Score 69.2;  DB 10;  Length 424;
  Best Local Similarity   56.6%;  Pred. No. 2.7e-05;
  Matches  128;  Conservative    0;  Mismatches   98;  Indels    0;  Gaps    0;

Qy    1093 TGTTTGAAGGATCTTATTTAAAATTGTTTTTGTATTTTCTTAAAGCAATATTCACTGTTA 1152
           | |||      || |  ||  ||  | ||||| ||| || |||||  |||||| |   ||
Db     247 TTTTTTTAAATTTCCTTATAATATTTTTTTTTATATTTTTAAACAAATATTTAAAATTT 188

Qy    1153 CACCTTGGGGACTTCTTTGTTTATCCATTCTTTTATCCTTTATATTTCATTTGTAAACTA 1212
           |  ||      || ||   || |   |  |||| |  ||| | |||  ||| ||   |
Db     187 TAATTTATTTTATTTTTAAATTTTTTTTATTTTTTTTATTTTTTTTTTTTTTTTATTTTT 128

Qy    1213 TATTTGAACGACATTCCCCCCGAAAAATTGAAATGTAAAGATGAGGCAGAGAATAAAGTG 1272
           | |||         ||        ||       |||   ||| |  |   | | || |||
Db     127 TTTTTTTTATTTTTTTATTTTTAATTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 68

Qy    1273 TTCTATGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1318
           |  ||||||||||||||||||||||||||||||||||||||||||||
Db      67 AAAAACCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 22


RESULT 10
```

US-09-746-359A-52
; Sequence 52, Application US/09746359A
; Patent No. US20020042366A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Penny
; APPLICANT: Foster, Donald C.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Madden, Karen L.
; APPLICANT: Kelly, James D.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Blumberg, Hal
; APPLICANT: Eagan, Maribeth A.
; APPLICANT: Jaspers, Stephen R.
; APPLICANT: Chandrasekher, Yasmin A.
; APPLICANT: No. US20020042366A1ak, Julia E.
; TITLE OF INVENTION: Method for Treating Inflammation
; FILE REFERENCE: 99-108
; CURRENT APPLICATION NUMBER: US/09/746,359A
; CURRENT FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/171,969
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/213,341
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 52
; LENGTH: 1720
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1713)
US-09-746-359A-52

Query Match 5.1%; Score 67; DB 10; Length 1720;
Best Local Similarity 51.5%; Pred. No. 0.00011;
Matches 154; Conservative 0; Mismatches 145; Indels 0; Gaps 0;

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Qy     529 AAATATGGACAGAGACAATGGAAAAATAAAGAAGACTGTTGGGGTACTCAAGAACTCTCT 588
           | |||||| || |   |||||   ||||||  ||| ||  |   ||   |   |  ||
Db     208 ATATATGGGCAAAAGAAATGGCTGAATAAATCAGAATGCAGAAATATCAATAGAACCTAC 267

Qy     589 TGTGACCTTACCAGTGAAACCTCAGACATACAGGAACCTTATTACGGGAGGGTGAGGGCG 648
           |||||  |||  |   ||||||  ||  |||     |  | |  |||||  |  |  ||  |  |||
Db     268 TGTGATCTTTCTGCTGAAACTTCTGACTACGAACACCAGTATTATGCCAAAGTTAAGGCC 327

Qy     649 GCCTCGGCTGGGAGCTACTCAGAATGGAGCATGACGCCGCGGTTCACTCCCTGGTGGGAA 708
           |  ||     |  |  ||  |||||      |     ||||||  |||  |  |  |||
Db     328 ATTTGGGGAACAAAGTGTTCCAAATGGGCTGAAAGTGGACGGTTCTATCCTTTTTTAGAA 387

Qy     709 ACAAAAATAGATCCTCCAGTCATGAATATAACCCAAGTCAATGGCTCTTTGTTGGTAATT 768
           |||  ||||  |  ||  ||||   ||    | ||   ||   |    ||  | |  ||  |
Db     388 ACACAAATTGGCCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTTCTGTTGTC 447

Qy     769 CTCCATGCTCCAAATTTACCATATAGATACCAAAAGGAAAAAAATGTATCTATAGAAGA 827
           ||    ||||||  |        | |||  |  |  |  ||      |||  ||  ||  ||  |
Db     448 CTGACAGCTCCAGAGAAGTGGAAGAGAAATCCAGAAGACCTTCCTGTTTCCATGCAACA 506
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RESULT 11
US-10-052-586-397
; Sequence 397, Application US/10052586
; Patent No. US20020127584A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Chen,Jian
; APPLICANT: Desnoyers,Luc
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Pan,James
; APPLICANT: Smith,Victoria
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C1
; CURRENT APPLICATION NUMBER: US/10/052,586
; CURRENT FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063564
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063734
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 60/063870
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066120
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/066466
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/066772
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/069335
; PRIOR FILING DATE: 1997-12-11
; PRIOR APPLICATION NUMBER: 60/069425
; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: 60/069870
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/068017
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/078886
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078939
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079664
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079786
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/080107
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080194
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080327
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080333
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/081049
; PRIOR FILING DATE: 1998-04-08

; PRIOR APPLICATION NUMBER: 60/081070
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081195
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081838
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082568
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082569
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082704
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082797
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/083495
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083496
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083499
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083559
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/084366
; PRIOR FILING DATE: 1998-05-05
; PRIOR APPLICATION NUMBER: 60/084414
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084639
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084640
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084643
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085582
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/086023
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/086392
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/086486
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087098
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087208
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087609
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087827
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: 60/088025
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088028
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088029
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088033
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088167
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088202
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088212
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088217
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088326
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088655
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: 60/088722
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088738
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088740
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088811
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088824
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088825
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088826
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088861
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; PRIOR APPLICATION NUMBER: 60/088863
; PRIOR FILING DATE: 1998-06-11
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; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/089090
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: 60/089105
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: 60/089512
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089514
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089538
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089598
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089653
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089908

Query Match 5.1%; Score 67; DB 12; Length 1750;
Best Local Similarity 51.5%; Pred. No. 0.00011;
Matches 154; Conservative 0; Mismatches 145; Indels 0; Gaps 0;

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Qy    709 ACAAAAATAGATCCTCCAGTCATGAATATAACCCAAGTCAATGGCTCTTTGTTGGTAATT 768
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RESULT 12
US-09-746-359A-22
; Sequence 22, Application US/09746359A
; Patent No. US20020042366A1
; GENERAL INFORMATION:

; APPLICANT: Thompson, Penny
; APPLICANT: Foster, Donald C.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Madden, Karen L.
; APPLICANT: Kelly, James D.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Blumberg, Hal
; APPLICANT: Eagan, Maribeth A.
; APPLICANT: Jaspers, Stephen R.
; APPLICANT: Chandrasekher, Yasmin A.
; APPLICANT: No. US20020042366Alak, Julia E.
; TITLE OF INVENTION: Method for Treating Inflammation
; FILE REFERENCE: 99-108
; CURRENT APPLICATION NUMBER: US/09/746,359A
; CURRENT FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/171,969
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/213,341
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 1801
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (8)...(1789)
US-09-746-359A-22

Query Match 5.1%; Score 67; DB 10; Length 1801;
Best Local Similarity 51.5%; Pred. No. 0.00011;
Matches 154; Conservative 0; Mismatches 145; Indels 0; Gaps 0;

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Db    248 ATATATGGGCAAAAGAAATGGCTGAATAAATCAGAATGCAGAAATATCAATAGAACCTAC 307

Qy    589 TGTGACCTTACCAGTGAAACCTCAGACATACAGGAACCTTATTACGGGAGGGTGAGGGCG 648
          |||||  |||  |   ||||||  || |||    |  | |  |||||  |  |  || | |||
Db    308 TGTGATCTTTCTGCTGAAACTTCTGACTACGAACACCAGTATTATGCCAAAGTTAAGGCC 367

Qy    649 GCCTCGGCTGGGAGCTACTCAGAATGGAGCATGACGCCGCGGTTCACTCCCTGGTGGGAA 708
          | ||     |  |  ||  |||||       |     ||||||  |||  |  |  |||
Db    368 ATTTGGGGAACAAAGTGTTCCAAATGGGCTGAAAGTGGACGGTTCTATCCTTTTTTAGAA 427

Qy    709 ACAAAAATAGATCCTCCAGTCATGAATATAACCCAAGTCAATGGCTCTTTGTTGGTAATT 768
          |||  ||||  |  ||  ||||   ||    | ||   ||   |    ||  |  |  ||  |
Db    428 ACACAAATTGGCCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTTCTGTTGTC 487

Qy    769 CTCCATGCTCCAAATTTACCATATAGATACCAAAAGGAAAAAAATGTATCTATAGAAGA 827
          ||    ||||||  |        | |||  |  |  |  |  ||       |||  ||  ||  || |
Db    488 CTGACAGCTCCAGAGAAGTGGAAGAGAAATCCAGAAGACCTTCCTGTTTCCATGCAACA 546
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RESULT 13
US-09-746-359A-10
; Sequence 10, Application US/09746359A
; Patent No. US20020042366A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Penny
; APPLICANT: Foster, Donald C.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Madden, Karen L.
; APPLICANT: Kelly, James D.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Blumberg, Hal
; APPLICANT: Eagan, Maribeth A.
; APPLICANT: Jaspers, Stephen R.
; APPLICANT: Chandrasekher, Yasmin A.
; APPLICANT: No. US20020042366A1ak, Julia E.
; TITLE OF INVENTION: Method for Treating Inflammation
; FILE REFERENCE: 99-108
; CURRENT APPLICATION NUMBER: US/09/746,359A
; CURRENT FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/171,969
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/213,341
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 3516
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (237)...(1895)
US-09-746-359A-10

Query Match 5.1%; Score 67; DB 10; Length 3516;
Best Local Similarity 51.5%; Pred. No. 0.00013;
Matches 154; Conservative 0; Mismatches 145; Indels 0; Gaps 0;

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Db    459 ATATATGGGCAAAAGAAATGGCTGAATAAATCAGAATGCAGAAATATCAATAGAACCTAC 518

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Db    519 TGTGATCTTTCTGCTGAAACTTCTGACTACGAACACCAGTATTATGCCAAAGTTAAGGCC 578

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Db    579 ATTTGGGGAACAAAGTGTTCCAAATGGGCTGAAAGTGGACGGTTCTATCCTTTTTTAGAA 638

Qy    709 ACAAAAATAGATCCTCCAGTCATGAATATAACCCAAGTCAATGGCTCTTTGTTGGTAATT 768
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Qy    769 CTCCATGCTCCAAATTTACCATATAGATACCAAAAGGAAAAAAATGTATCTATAGAAGA 827
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Db    699 CTGACAGCTCCAGAGAAGTGGAAGAGAAATCCAGAAGACCTTCCTGTTTCCATGCAACA 757
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RESULT 14
US-09-960-352-12673/c
; Sequence 12673, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 12673
; LENGTH: 277
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 54-LIB3058-039-Q1-K1-F10
US-09-960-352-12673

Query Match 5.0%; Score 66.2; DB 10; Length 277;
Best Local Similarity 54.8%; Pred. No. 9.4e-05;
Matches 131; Conservative 0; Mismatches 108; Indels 0; Gaps 0;

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RESULT 15
US-09-960-352-15014/c
; Sequence 15014, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
;  APPLICANT: Warren, Wesley C.
;  APPLICANT:  Tao, Nengbing
;  APPLICANT:  Byatt, John C.
;  APPLICANT:  Mathialagan, Nagappan
;  TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
;  TITLE OF INVENTION:  MUSCLE AND FAT DEPOSITION
;  FILE REFERENCE: 16511.006/37-21(10298)C
;  CURRENT APPLICATION NUMBER: US/09/960,352
;  CURRENT FILING DATE:  2001-09-24
;  NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 15014
;   LENGTH: 375
;   TYPE: DNA
;   ORGANISM: Bos taurus
;   OTHER INFORMATION: Clone ID: 64-LIB3058-048-Q1-K1-H8
US-09-960-352-15014

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  Matches  120;  Conservative    0;  Mismatches   93;  Indels    0;  Gaps    0;

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Qy   1166 TCTTTGTTTATCCATTCTTTTATCCTTTATATTTCATTTGTAAACTATATTTGAACGACA 1225
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Qy   1226 TTCCCCCCGAAAAATTGAAATGTAAAGATGAGGCAGAGAATAAAGTGTTCTATGAAAAAA 1285
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GenCore version 5.1.3

OM protein - protein search, using sw model

Run on: December 22, 2002, 09:11:22 ; Search time 67 Seconds
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Perfect score: 1427
Sequence: 1 MPKHCFLGFLISFFLTGVAG.....YQPMLDRRSQRSEERCVEIP 262

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1427	100.0	262	22	AAU09186	Human PRO19598 pol
2	1427	100.0	263	23	AAE17321	Human cytokine rec
3	1423	99.7	263	23	AAO17382	Human cytokine rec
4	1392	97.5	263	23	AAU80324	Human IL-TIF/IL-22
5	1213	85.0	231	22	AAE05048	Human ZCYTO18 solu
6	1213	85.0	231	22	AAE02460	Human DNAX cytokin
7	1213	85.0	231	22	AAB62657	Human cytokine rec
8	1213	85.0	231	23	AAO17381	Human cytokine rec
9	1213	85.0	231	23	AAU80000	Human IL-TIF/IL-22
10	1213	85.0	231	23	ABG34086	Human Pro peptide
11	1213	85.0	231	23	AAE17320	Human cytokine rec
12	1114	78.1	214	23	AAE17319	Human cytokine rec
13	1104	77.4	210	22	AAB62663	Human zcytor16 ext
14	1045	73.2	249	22	AAE02458	Human DNAX cytokin
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18	310	21.7	207	23	ABG67220	Interleukin-20 sub
19	310	21.7	214	22	AAB85287	Human IL-20 recept
20	310	21.7	214	23	ABG67218	Interleukin-20 sub
21	310	21.7	217	22	AAB85280	IL-20RA-Ig gamma1
22	310	21.7	217	23	ABG67211	Interleukin-20 sub
23	310	21.7	221	22	AAB85269	Human IL-20 recept
24	310	21.7	221	23	ABG67200	Human Interleukin-
25	310	21.7	221	23	AAE23354	Human IL-20RA matu
26	310	21.7	542	22	AAU29222	Human PRO polypept
27	310	21.7	542	22	AAU12265	Human PRO4978 poly
28	310	21.7	547	22	AAB85279	Human IL-20RA-Ig g
29	310	21.7	547	23	ABG67210	Interleukin-20RB/I
30	310	21.7	547	23	AAE23362	Human IL-20RA EC d
31	310	21.7	553	19	AAW79159	Zcytor7 cytokine r
32	310	21.7	553	22	ABB11582	Human class II cyt
33	310	21.7	553	22	AAU04058	Human interleukin-
34	310	21.7	553	22	AAB85268	Human IL-20 recept
35	310	21.7	553	23	ABG67199	Human Interleukin-
36	310	21.7	553	23	AAE23353	Human interleukin-
37	310	21.7	555	22	AAU04072	Human IL-20RA/immu
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39	310	21.7	559	23	ABG67217	IL-20RA extracellu
40	310	21.7	559	23	AAE23361	Human IL-20RA EC d
41	310	21.7	571	22	AAU04065	Human IL-20RA/immu
42	310	21.7	571	22	AAB85278	Human IL-20RA-Ig g
43	310	21.7	571	23	ABG67209	Interleukin-20RB/I
44	310	21.7	571	23	AAE23359	Human IL-20RA extr
45	310	21.7	594	22	AAU04062	Human IL-20RA/immu

ALIGNMENTS

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ID AAU09186 standard; Protein; 262 AA.
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AC AAU09186;
XX
DT 16-JAN-2002 (first entry)
XX
DE Human PRO19598 polypeptide.
XX
KW Human; PRO19598; clone DNA145887; immune-related disorder;
KW inflammatory disorder; infectious disorder; immunodeficiency disorder;
KW autoimmune disorder; renal disease; demyelinating disease; skin disease;
KW neoplasia; transplantation associated disease; immunosuppressive;
KW anti-inflammatory; antiasthmatic; antidiabetic.
XX
OS Homo sapiens.
XX

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FT Modified-site 220..225
FT /note= "N-myristoylation site"
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PD 13-SEP-2001.
XX
PF 01-MAR-2001; 2001WO-US06666.
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PR 03-MAR-2000; 2000US-187202P.
PR 21-MAR-2000; 2000US-191015P.
PR 30-MAY-2000; 2000WO-US14941.
PR 05-JUN-2000; 2000US-209832P.
PR 24-AUG-2000; 2000WO-US23328.
PR 01-DEC-2000; 2000WO-US32678.
XX
PA (GETH) GENENTECH INC.
XX
PI Eaton DL, Fong S, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL;
PI Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2001-625876/72.
DR N-PSDB; AAS15368.
XX
PT Nucleic acids encoding PRO polypeptides, useful for detecting and
PT treating immune related diseases and disorders in mammals including
PT autoimmune diseases, inflammatory diseases and asthma -
XX
PS Claim 10; Fig 18; 122pp; English.
XX
CC The present invention relates to the isolation of 9 novel human PRO
CC polypeptides and the cDNA sequences (AAS15360-AAS15368) encoding them.
CC The novel PRO polypeptides include PRO1356, PRO1268, PRO1884, PRO3444,
CC PRO3151, PRO4322, PRO9964, PRO10008 and PRO19598. The cDNA sequences
CC encoding these PRO polypeptides have been designated as clones
CC DNA64886-1601, DNA64903-1553, DNA84318-2520, DNA87997, DNA89273,
CC DNA92223-2567, DNA96973, DNA101921 and DNA145887 respectively.
CC Compositions (e.g. vaccines) containing PRO polypeptides and methods of
CC using these compositions are useful in the treatment and diagnosis of
CC immune-related disorders. Such disorders include immune-mediated
CC inflammatory disorders (e.g. osteoarthritis), non-immune-mediated
CC inflammatory disorders (e.g. diabetes mellitus), infectious disorders
CC (e.g. granulomatous hepatitis), immunodeficiency disorders (e.g. AIDS),
CC autoimmune disorders (e.g. rheumatoid arthritis), immune-related renal
CC diseases (e.g. cirrhosis), demyelinating diseases of the peripheral or
CC central nervous system (e.g. Guillain-Barre syndrome), immune-mediated
CC skin diseases (e.g. contact dermatitis), neoplasias and transplantation
CC associated diseases. The polynucleotide sequences of the invention may
CC be used in gene therapy. AAU09178-AAU09186 represent the novel human
CC PRO polypeptides of the invention.
XX
SQ Sequence 262 AA;

Query Match 100.0%; Score 1427; DB 22; Length 262;
Best Local Similarity 100.0%; Pred. No. 2.4e-134;
Matches 262; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 MPKHCFLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVYF 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MPKHCFLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVYF 60

Qy     61 VQYKIMFSCSMKSSHQKPSGCWQHISCNFPGCRTLAKYGQRQWKNKEDCWGTQELSCDLT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 VQYKIMFSCSMKSSHQKPSGCWQHISCNFPGCRTLAKYGQRQWKNKEDCWGTQELSCDLT 120

Qy    121 SETSDIQEPYYGRVRAASAGSYSEWSMTPRFTPWWETKIDPPVMNITQVNGSLLVILHAP 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 SETSDIQEPYYGRVRAASAGSYSEWSMTPRFTPWWETKIDPPVMNITQVNGSLLVILHAP 180

Qy    181 NLPYRYQKEKNVSIEDYYELLYRVFIINNSLEKEQKVYEGAHRAVEIEALTPHSSYCVVA 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 NLPYRYQKEKNVSIEDYYELLYRVFIINNSLEKEQKVYEGAHRAVEIEALTPHSSYCVVA 240

Qy    241 EIYQPMLDRRSQRSEERCVEIP 262
          |||||||||||||||||||||||
Db    241 EIYQPMLDRRSQRSEERCVEIP 262
```

RESULT 2
AAE17321
ID AAE17321 standard; Protein; 263 AA.
XX
AC AAE17321;
XX
DT 18-APR-2002 (first entry)
XX
DE Human cytokine receptor protein, sbg456548CytoRa #3.
XX
KW Human; therapy; wound healing disorder; vaccine; cancer; infection;
KW autoimmune disorder; haematopoietic disorder; inflammation; arthritis;
KW Parkinson's disease; Huntington's chorea; schizophrenia; antiarrhythmic;
KW multiple sclerosis; Alzheimer's disease; analgesic; cardiant; asthma;
KW ischaemia; stroke; AIDS; bone disease; atherosclerosis; brain disorder;
KW depression; cardiovascular disease; myocardial infarction; renal failure;
KW respiratory disease; liver disorder; Fanconi's syndrome; spleen disorder;
KW type II diabetes mellitus; skeletal muscle disorder; immunosuppressive;
KW hypersplenism; renal disease; hypoglycaemia; gastrointestinal disease;
KW nootropic; cirrhosis; Hodgkin's disease; neuroleptic; antiinflammatory;
KW haemostatic; vulnerary; anticonvulsant; antirheumatic; neuroprotective;
KW nephrotropic; hypotensive; vasotropic; cytostatic; cerebroprotective;
KW allergy; cytokine receptor.
XX
OS Homo sapiens.
XX
PN WO200198342-A1.
XX
PD 27-DEC-2001.
XX
PF 22-JUN-2001; 2001WO-US19929.
XX
PR 22-JUN-2000; 2000US-213156P.
PR 22-JUN-2000; 2000US-213161P.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PA (GLAX) GLAXO GROUP LTD.
XX
PI Agarwal P, Cogswell JP, Kabnic KS, Lai Y, Martensen SA;
PI Murdock PR, Smith RF, Strum JC, Xiang Z, Xie Q, Rizni SK;
XX
DR WPI; 2002-139783/18.
DR N-PSDB; AAD27816.
XX
PT Novel secreted and membrane-associated polypeptides and polynucleotides
PT useful for preventing, ameliorating or correcting dysfunction or
PT disease including diabetes, cancer, hypertension and growth
PT abnormalities -
XX
PS Claim 1; Page 133-134; 138pp; English.
XX
CC The invention relates to secreted and membrane-associated polypeptides
CC and polynucleotides. The sequences of the invention are useful in
CC diagnostic assays for detecting diseases associated with inappropriate
CC activity or levels of these polynucleotides, and in identifying their
CC agonists and antagonists that are potentially useful in therapy. The
CC sequences of the invention are useful as vaccines for inducing
CC immunological response. The sequences of the invention are useful for
CC treating cancers, infections, autoimmune disorders, haematopoietic
CC disorders, wound healing disorders, cholesteryl ester storage disease,
CC inflammation, congenital muscular dystrophy, junctional epidermolysis
CC bullosa, Parkinson's disease, Huntington's chorea, multiple sclerosis,
CC viral and bacterial infections, Alzheimer's disease, asthma, arthritis,

CC allergies, schizophrenia, sbg442445PROa-associated disorders,
CC septicaemia, psoriasis, inflammatory bowel disease, transplant rejection,
CC graft verse host disease, ischaemia, stroke, acute respiratory disease
CC syndrome, restenosis, brain injury, AIDS, bone diseases, atherosclerosis,
CC brain disorders including parasupranuclear palsy, myotonic dystrophy,
CC depression, anxiety disorders and sleep disorders, cardiovascular
CC diseases including congestive heart failure and myocardial infarction,
CC respiratory diseases including chronic obstructive pulmonary disease,
CC acute bronchitis and adult respiratory distress syndrome, liver disorders
CC including hypercholesterolaemia, hypertriglyceridaemia, cirrhosis, viral
CC and non-viral hepatitis, type II diabetes mellitus, renal disease
CC including acute and chronic renal failure, glomerulonephritis, Fanconi's
CC syndrome, cystinuria, skeletal muscle disorders including hypoglycaemia
CC and tendinitis, gastrointestinal diseases including intestinal
CC obstruction and tropical sprue, spleen disorders including hypersplenism,
CC Hodgkin's disease and malignant lymphoma, testicular cancer, male
CC reproductive diseases including low testosterone and male infertility.
CC The present sequence is human cytokine receptor.
XX
SQ Sequence 263 AA;

Query Match 100.0%; Score 1427; DB 23; Length 263;
Best Local Similarity 100.0%; Pred. No. 2.4e-134;
Matches 262; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1 MPKHCFLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVYF 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2 MPKHCFLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVYF 61

Qy      61 VQYKIMFSCSMKSSHQKPSGCWQHISCNFPGCRTLAKYGQRQWKNKEDCWGTQELSCDLT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      62 VQYKIMFSCSMKSSHQKPSGCWQHISCNFPGCRTLAKYGQRQWKNKEDCWGTQELSCDLT 121

Qy     121 SETSDIQEPYYGRVRAASAGSYSEWSMTPRFTPWWETKIDPPVMNITQVNGSLLVILHAP 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     122 SETSDIQEPYYGRVRAASAGSYSEWSMTPRFTPWWETKIDPPVMNITQVNGSLLVILHAP 181

Qy     181 NLPYRYQKEKNVSIEDYYELLYRVFIINNSLEKEQKVYEGAHRAVEIEALTPHSSYCVVA 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     182 NLPYRYQKEKNVSIEDYYELLYRVFIINNSLEKEQKVYEGAHRAVEIEALTPHSSYCVVA 241

Qy     241 EIYQPMLDRRSQRSEERCVEIP 262
          |||||||||||||||||||||||
Db     242 EIYQPMLDRRSQRSEERCVEIP 263
```

RESULT 3
AAO17382
ID AAO17382 standard; Protein; 263 AA.
XX
AC AAO17382;
XX
DT 08-AUG-2002 (first entry)
XX
DE Human cytokine receptor variant 3.
XX
KW Human; cytokine receptor; immune disease; psoriasis; cancer; infection;
KW rheumatoid arthritis; multiple sclerosis; Crohn's disease;
KW ulcerative colitis; transplant rejection; abortion; antipsoriatic;
KW immunosuppressive; antirheumatic; antiarthritic; neuroprotective;
KW antiinflammatory; antiulcer; cytostatic; dermatological;
KW chromosome 6q24.1-25.2; receptor.
XX
OS Homo sapiens.
XX
PN EP1191035-A2.
XX
PD 27-MAR-2002.
XX
PF 24-AUG-2001; 2001EP-0250307.
XX
PR 25-SEP-2000; 2000DE-1048626.
PR 17-NOV-2000; 2000DE-1058907.
PR 19-DEC-2000; 2000DE-1064906.
XX
PA (SCHD) SCHERING AG.
XX
PI Weiss B, Sabat R, Assadullah K, Toshi L;
XX
DR WPI; 2002-332210/37.
DR N-PSDB; AAL46001.
XX
PT New nucleic acid encoding soluble cytokine receptor, useful for
PT diagnosis and treatment of e.g. immune disease, also related protein
PT and antibodies -
XX
PS Claim 6; Page 15; 21pp; German.
XX
CC The present invention provides the protein and coding sequences of 3
CC variants of a human cytokine receptor. The sequences can be used in the
CC diagnosis, prevention and treatment of immune diseases, including
CC psoriasis, cancer, chronic/life-threatening infections, rheumatoid
CC arthritis, multiple sclerosis, Crohn's disease, ulcerative colitis and
CC transplant rejection and in reproductive medicine, e.g. for diagnosing
CC abnormal immune reactions which cause abortions. The present sequence is
CC variant 3 of the invention.
XX
SQ Sequence 263 AA;

Query Match 99.7%; Score 1423; DB 23; Length 263;
Best Local Similarity 99.6%; Pred. No. 6e-134;
Matches 261; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1 MPKHCFLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVYF 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2 MPKHCFLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVYF 61

Qy      61 VQYKIMFSCSMKSSHQKPSGCWQHISCNFPGCRTLAKYGQRQWKNKEDCWGTQELSCDLT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      62 VQYKIMFSCSMKSSHQKPSGCWQHISCNFPGCRTLAKYGQRQWKNKEDCWGTQELSCDLT 121

Qy     121 SETSDIQEPYYGRVRAASAGSYSEWSMTPRFTPWWETKIDPPVMNITQVNGSLLVILHAP 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     122 SETSDIQEPYYGRVRAASAGSYSEWSMTPRFTPWWETKIDPPVMNITQVNGSLLVILHAP 181

Qy     181 NLPYRYQKEKNVSIEDYYELLYRVFIINNSLEKEQKVYEGAHRAVEIEALTPHSSYCVVA 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     182 NLPYRYQKEKNVSIEDYYELLYRVFIINNSLEKEQKVYEGAHRAVEIEALTPHSSYCVVA 241

Qy     241 EIYQPMLDRRSQRSEERCVEIP 262
          |||||||||||:|||||||||||
Db     242 EIYQPMLDRRSRRSEERCVEIP 263
```

RESULT 4
AAU80324
ID AAU80324 standard; Protein; 263 AA.
XX
AC AAU80324;
XX
DT 15-JUL-2002 (first entry)
XX
DE Human IL-TIF/IL-22 binding protein #2.
XX
KW Human; soluble protein; interleukin-TIF/IL-22; IL-TIF/IL-22; IL-22BP;
KW IL-TIF/IL-22 antagonist.
XX
OS Homo sapiens.
XX
PN WO200224912-A2.
XX
PD 28-MAR-2002.
XX
PF 21-SEP-2001; 2001WO-US29576.
XX
PR 22-SEP-2000; 2000US-234583P.

PR 03-NOV-2000; 2000US-245495P.
PR 31-JUL-2001; 2001US-0919162.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Renauld J, Dumoutier L;
XX
DR WPI; 2002-383190/41.
DR N-PSDB; ABK50080.
XX
PT Polynucleotide and polypeptide of soluble protein which binds to
PT interleukin-TIF/IL-22 useful for inhibiting effect of IL-TIF/IL-22 on a
PT cell -
XX
PS Claim 14; Page 41-42; 42pp; English.
XX
CC The present invention relates to a new polynucleotide that encodes a
CC soluble protein which binds to interleukin (IL)-TIF/IL-22 (also referred
CC to as IL-22BP), where the complementary sequence of the invention
CC hybridises under stringent conditions to a nucleotide sequence of 2271
CC or 2366 base pairs, as given in the specification. The molecules of the
CC invention are useful for inhibiting (antagonising) effect of IL-TIF/IL-22
CC on a cell, for determining whether IL-TIF/IL-22 is present in a sample,
CC for inhibiting binding of IL-TIF/IL-22 to a binding partner, preferably
CC in vitro, and for obtaining an antibody molecule specific for the soluble
CC binding protein of the invention, from a population or panel of antibody
CC molecules of diverse binding specificity. The soluble protein is further
CC useful in manufacture of a medicament for treating an IL-22 mediated
CC disease and for assaying an agent, preferably an antibody or a peptide
CC fragment of IL-TIF/IL-22 or the soluble protein, that modulates binding
CC of the soluble protein to IL-TIF/IL-22, where the agent identified is
CC used in the manufacture of medicament for treating IL-TIF/IL-22 mediated
CC disorder. The antibody is useful for determining presence of the soluble
CC protein, where the antibody is detectably labelled. The present amino
CC acid sequence represents the human IL-TIF/IL-22 binding protein #2 of
CC the invention.
XX
SQ Sequence 263 AA;

Query Match 97.5%; Score 1392; DB 23; Length 263;
Best Local Similarity 98.1%; Pred. No. 7.6e-131;
Matches 257; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```
Qy       1 MPKHCFLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVYF 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2 MPKHCFLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVYF 61

Qy      61 VQYKIMFSCSMKSSHQKPSGCWQHISCNFPGCRTLAKYGQRQWKNKEDCWGTQELSCDLT 120
          |||||||||||||||     ||||||||||||||||||||||||||||||||||||||||||
Db      62 VQYKIMFSCSMKSSHQSQVDAWQHISCNFPGCRTLAKYGQRQWKNKEDCWGTQELSCDLT 121

Qy     121 SETSDIQEPYYGRVRAASAGSYSEWSMTPRFTPWWETKIDPPVMNITQVNGSLLVILHAP 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     122 SETSDIQEPYYGRVRAASAGSYSEWSMTPRFTPWWETKIDPPVMNITQVNGSLLVILHAP 181

Qy     181 NLPYRYQKEKNVSIEDYYELLYRVFIINNSLEKEQKVYEGAHRAVEIEALTPHSSYCVVA 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     182 NLPYRYQKEKNVSIEDYYELLYRVFIINNSLEKEQKVYEGAHRAVEIEALTPHSSYCVVA 241

Qy     241 EIYQPMLDRRSQRSEERCVEIP 262
          |||||||||||||||||||||||
Db     242 EIYQPMLDRRSQRSEERCVEIP 263
```

RESULT 5
AAE05048
ID AAE05048 standard; Protein; 231 AA.
XX
AC AAE05048;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human ZCYTO18 soluble receptor antagonist, zcytor16 protein.
XX
KW Human; cytostatic; cytokine; ZCYTO18 protein; genetic abnormality;
KW cancer; inflammation; gene therapy; zcytor16.
XX
OS Homo sapiens.
XX
PN WO200146422-A1.
XX
PD 28-JUN-2001.
XX
PF 22-DEC-2000; 2000WO-US35308.
XX
PR 23-DEC-1999; 99US-0471767.
PR 01-DEC-2000; 2000US-0250841.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Presnell SR, Kindsvogel W;
XX
DR WPI; 2001-408648/43.
DR N-PSDB; AAD09745.
XX
PT Novel human cytokine polypeptide, ZCYTO18, useful for treating cancer -
XX
PS Example 13A; Page 158-159; 167pp; English.
XX
CC The patent discloses novel human cytokine, ZCYTO18 protein and its
CC corresponding DNA. ZCYTO18 protein induces proliferation of cells
CC expressing zcytor11, a receptor for ZCYTO18 or induces cytotoxicity
CC in K5626 cells. ZCYTO18 DNA is useful for detecting a genetic
CC abnormality in a patient. ZCYTO18 DNA and its antibodies are useful
CC for detecting cancer and inflammation. ZCYTO18 protein is useful for
CC killing cancer cells. It is useful for increasing platelets in a
CC patient or injured tissue. It is also used in gene therapy.
CC The present sequence is human zcytor16, which is a naturally expressed
CC soluble receptor antagonist of ZCYTO18 protein.
XX
SQ Sequence 231 AA;

Query Match 85.0%; Score 1213; DB 22; Length 231;
Best Local Similarity 87.8%; Pred. No. 5.2e-113;
Matches 230; Conservative 0; Mismatches 0; Indels 32; Gaps 1;

```
Qy       1 MPKHCFLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVYF 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2 MPKHCFLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVYF 61

Qy      61 VQYKIMFSCSMKSSHQKPSGCWQHISCNFPGCRTLAKYGQRQWKNKEDCWGTQELSCDLT 120
          |||||                              ||||||||||||||||||||||
Db      62 VQYKI------------------------------YGQRQWKNKEDCWGTQELSCDLT 89

Qy     121 SETSDIQEPYYGRVRAASAGSYSEWSMTPRFTPWWETKIDPPVMNITQVNGSLLVILHAP 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      90 SETSDIQEPYYGRVRAASAGSYSEWSMTPRFTPWWETKIDPPVMNITQVNGSLLVILHAP 149

Qy     181 NLPYRYQKEKNVSIEDYYELLYRVFIINNSLEKEQKVYEGAHRAVEIEALTPHSSYCVVA 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     150 NLPYRYQKEKNVSIEDYYELLYRVFIINNSLEKEQKVYEGAHRAVEIEALTPHSSYCVVA 209

Qy     241 EIYQPMLDRRSQRSEERCVEIP 262
          |||||||||||||||||||||||
Db     210 EIYQPMLDRRSQRSEERCVEIP 231
```

RESULT 6
AAE02460
ID AAE02460 standard; Protein; 231 AA.
XX
AC AAE02460;
XX
DT 10-AUG-2001 (first entry)
XX
DE Human DNAX cytokine receptor subunit 4.2 (DCRS4.2).

XX
KW Human; immunomodulator; DNAX cytokine receptor subunit 4.2; DCRS4.2;
KW therapy; immunological disorder; drug screening; cell development;
KW chromosome 6q24.1-25.2.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..21
FT /label= Signal-peptide
FT Protein 22..231
FT /label= DCRS4.2
FT /note= "Human mature DNAX cytokine receptor
FT subunit 4.2"
XX
PN WO200136467-A2.
XX
PD 25-MAY-2001.
XX
[redacted] 16-NOV-2000; 2000WO-US31363.

[redacted] 18-NOV-1999; 99US-0443060.
PR 13-DEC-1999; 99US-0170320.
XX
PA (SCHE) SCHERING CORP.
XX
PI Gorman DM;
XX
DR WPI; 2001-343800/36.
DR N-PSDB; AAD06414.
XX
PT New mammalian receptor proteins related to cytokine receptors, useful
PT for regulating cell development and for diagnosis and treatment of
PT immunological disorders -
XX
PS Claim 3; Page 23; 124pp; English.
XX
CC The present sequence is human DNAX cytokine receptor subunit 4.2
CC (DCRS4.2). DCRS4 gene is located on chromosome 6q24.1-25.2.
CC Cytokine receptors, fragments and antibodies are useful for treating
CC immunological disorders. DCRS3 (50R), DCRS4 (cytor) or fragments are
CC useful in drug screening to identify compounds having binding affinity
CC to the receptor subunit. Modulators of DCRS are useful for modulating
CC the physiology or development of a cell or tissue culture cells. A
CC purified DCRS is useful as a reagent to detect antibodies generated in
CC response to the presence of elevated levels of expression, or
CC immunological disorders which lead to production of antibody to the
CC endogenous receptor. Cytokine receptor sequences are useful as probes
CC for detecting levels of the cytokine receptor in patients suspected of
CC having an immunological disorder. Antibodies have therapeutic value, are
CC useful as potent antagonist, in detecting or quantifying ligands, for
CC isolating DCRS proteins and peptides, to screen expression libraries for
CC particular expression products, to raise anti-idiotypic antibodies and
CC for detecting or diagnosing various immunological conditions related to
CC expression of the protein or cells which express the protein.
XX
SQ Sequence 231 AA;

Query Match 85.0%; Score 1213; DB 22; Length 231;
Best Local Similarity 87.8%; Pred. No. 5.2e-113;
Matches 230; Conservative 0; Mismatches 0; Indels 32; Gaps 1;

```
Qy       1 MPKHCFLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVYF 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2 MPKHCFLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVYF 61

Qy      61 VQYKIMFSCSMKSSHQKPSGCWQHISCNFPGCRTLAKYGQRQWKNKEDCWGTQELSCDLT 120
           |||||                                ||||||||||||||||||||||
Db      62 VQYKI--------------------------------YGQRQWKNKEDCWGTQELSCDLT 89

Qy     121 SETSDIQEPYYGRVRAASAGSYSEWSMTPRFTPWWETKIDPPVMNITQVNGSLLVILHAP 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      90 SETSDIQEPYYGRVRAASAGSYSEWSMTPRFTPWWETKIDPPVMNITQVNGSLLVILHAP 149

Qy     181 NLPYRYQKEKNVSIEDYYELLYRVFIINNSLEKEQKVYEGAHRAVEIEALTPHSSYCVVA 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     150 NLPYRYQKEKNVSIEDYYELLYRVFIINNSLEKEQKVYEGAHRAVEIEALTPHSSYCVVA 209

Qy     241 EIYQPMLDRRSQRSEERCVEIP 262
           |||||||||||||||||||||||
Db     210 EIYQPMLDRRSQRSEERCVEIP 231
```

RESULT 7
AAB62657
ID AAB62657 standard; Protein; 231 AA.
XX
AC AAB62657;
XX
DT 23-JUL-2001 (first entry)
XX
DE Human cytokine receptor, zcytor16.
XX
KW Cytokine receptor; zcytor16; IL-TIF; antiinflammatory; cytostatic;
KW antirheumatic; antiarthritic; antiasthmatic; antiatherosclerotic;
KW immunosuppressive; chromosome 6q24.1-25.2; human.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 22..108
FT /note= "Ig domain 1"
FT Domain 22..231
FT /note= "extracellular domain"
FT Domain 112..210
FT /note= "Ig domain 2"
XX
PN WO200140467-A1.
XX
PD 07-JUN-2001.
XX
PF 01-DEC-2000; 2000WO-US32703.
XX
PR 03-DEC-1999; 99US-0169049.
PR 13-SEP-2000; 2000US-0232219.
PR 31-OCT-2000; 2000US-0244610.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Presnell SR, Xu W, Kindsvogel W, Chen Z;
XX
DR WPI; 2001-356158/37.
DR N-PSDB; AAF83735.
XX
PT New soluble cytokine receptor polypeptides and polynucleotides, useful
PT for diagnosing and treating cancer and inflammatory conditions -
XX
PS Claim 1; Page 186-188; 210pp; English.
XX
CC The invention relates to a human cytokine receptor polypeptide,
CC designated zcytor16. The zcytor16 polypeptide can be expressed by
CC standard recombinant methodology and can bind to IL-TIF (undefined). The
CC zcytor16 protein is useful for: inhibiting IL-TIF induced proliferation
CC or differentiation of hematopoietic cell(s) (progenitors); reducing
CC IL-TIF induced or IL-9 induced inflammation; and suppressing an
CC inflammatory response in a mammal with inflammation. Heteromeric/
CC multimeric receptor polypeptides such as soluble zcytor 16/CRF2-4 can be
CC used to reduce progression and symptoms of cancer. Zcytor16 polypeptides
CC can also be used to detect IL-TIF levels which is indicative of
CC pathological conditions including inflammatory states (e.g. rheumatoid
CC arthritis) and cancer. Antibodies that bind zcytor16 polypeptides and the
CC polypeptides themselves are useful for the treatment of inflammation,
CC inflammatory diseases (e.g. infection, asthma, inflammatory bowel
CC disease, rheumatoid arthritis and atherosclerosis) and autoimmune
CC diseases. The antibodies and zcytor16 polynucleotides are also useful
CC for detecting cancer. The present sequence represents the human

```
CC   zcytor16 protein.
XX
SQ   Sequence   231 AA;

  Query Match             85.0%;  Score 1213;  DB 22;  Length 231;
  Best Local Similarity   87.8%;  Pred. No. 5.2e-113;
  Matches  230;  Conservative    0;  Mismatches    0;  Indels   32;  Gaps    1;

Qy       1 MPKHCFLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVYF 60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2 MPKHCFLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVYF 61

Qy      61 VQYKIMFSCSMKSSHQKPSGCWQHISCNFPGCRTLAKYGQRQWKNKEDCWGTQELSCDLT 120
           |||||                                |||||||||||||||||||||
Db      62 VQYKI--------------------------------YGQRQWKNKEDCWGTQELSCDLT 89

Qy     121 SETSDIQEPYYGRVRAASAGSYSEWSMTPRFTPWWETKIDPPVMNITQVNGSLLVILHAP 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      90 SETSDIQEPYYGRVRAASAGSYSEWSMTPRFTPWWETKIDPPVMNITQVNGSLLVILHAP 149

Qy     181 NLPYRYQKEKNVSIEDYYELLYRVFIINNSLEKEQKVYEGAHRAVEIEALTPHSSYCVVA 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     150 NLPYRYQKEKNVSIEDYYELLYRVFIINNSLEKEQKVYEGAHRAVEIEALTPHSSYCVVA 209

Qy     241 EIYQPMLDRRSQRSEERCVEIP 262
           |||||||||||||||||||||||
Db     210 EIYQPMLDRRSQRSEERCVEIP 231


RESULT 8
AAO17381
ID   AAO17381 standard; Protein; 231 AA.
XX
AC   AAO17381;
XX
DT   08-AUG-2002  (first entry)
XX
DE   Human cytokine receptor variant 2.
XX
KW   Human; cytokine receptor; immune disease; psoriasis; cancer; infection;
KW   rheumatoid arthritis; multiple sclerosis; Crohn's disease;
KW   ulcerative colitis; transplant rejection; abortion; antipsoriatic;
KW   immunosuppressive; antirheumatic; antiarthritic; neuroprotective;
KW   antiinflammatory; antiulcer; cytostatic; dermatological;
KW   chromosome 6q24.1-25.2; receptor.
XX
OS   Homo sapiens.
XX
PN   EP1191035-A2.
XX
PD   27-MAR-2002.
XX
PF   24-AUG-2001; 2001EP-0250307.
XX
PR   25-SEP-2000; 2000DE-1048626.
PR   17-NOV-2000; 2000DE-1058907.
PR   19-DEC-2000; 2000DE-1064906.
XX
PA   (SCHD ) SCHERING AG.
XX
PI   Weiss B,  Sabat R,  Assadullah K,  Toshi L;
XX
DR   WPI; 2002-332210/37.
DR   N-PSDB; AAL46000.
XX
PT   New nucleic acid encoding soluble cytokine receptor, useful for
PT   diagnosis and treatment of e.g. immune disease, also related protein
PT   and antibodies  -
XX
PS   Claim 6; Page 14; 21pp; German.
XX
CC   The present invention provides the protein and coding sequences of 3
CC   variants of a human cytokine receptor. The sequences can be used in the
CC   diagnosis, prevention and treatment of immune diseases, including
CC   psoriasis, cancer, chronic/life-threatening infections, rheumatoid
CC   arthritis, multiple sclerosis, Crohn's disease, ulcerative colitis and
CC   transplant rejection and in reproductive medicine, e.g. for diagnosing
CC   abnormal immune reactions which cause abortions. The present sequence is
CC   variant 2 of the invention.
XX
SQ   Sequence   231 AA;

  Query Match             85.0%;  Score 1213;  DB 23;  Length 231;
  Best Local Similarity   87.8%;  Pred. No. 5.2e-113;
  Matches  230;  Conservative    0;  Mismatches    0;  Indels   32;  Gaps    1;

Qy       1 MPKHCFLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVYF 60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2 MPKHCFLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVYF 61

Qy      61 VQYKIMFSCSMKSSHQKPSGCWQHISCNFPGCRTLAKYGQRQWKNKEDCWGTQELSCDLT 120
           |||||                                |||||||||||||||||||||
Db      62 VQYKI--------------------------------YGQRQWKNKEDCWGTQELSCDLT 89

Qy     121 SETSDIQEPYYGRVRAASAGSYSEWSMTPRFTPWWETKIDPPVMNITQVNGSLLVILHAP 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      90 SETSDIQEPYYGRVRAASAGSYSEWSMTPRFTPWWETKIDPPVMNITQVNGSLLVILHAP 149

Qy     181 NLPYRYQKEKNVSIEDYYELLYRVFIINNSLEKEQKVYEGAHRAVEIEALTPHSSYCVVA 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     150 NLPYRYQKEKNVSIEDYYELLYRVFIINNSLEKEQKVYEGAHRAVEIEALTPHSSYCVVA 209

Qy     241 EIYQPMLDRRSQRSEERCVEIP 262
           |||||||||||||||||||||||
Db     210 EIYQPMLDRRSQRSEERCVEIP 231


RESULT 9
AAU80000
ID   AAU80000 standard; Protein; 231 AA.
XX
AC   AAU80000;
XX
DT   15-JUL-2002  (first entry)
XX
DE   Human IL-TIF/IL-22 binding protein #1.
XX
KW   Human; soluble protein; interleukin-TIF/IL-22; IL-TIF/IL-22; IL-22BP;
KW   IL-TIF/IL-22 antagonist.
XX
OS   Homo sapiens.
XX
PN   WO200224912-A2.
XX
PD   28-MAR-2002.
XX
PF   21-SEP-2001; 2001WO-US29576.
XX
PR   22-SEP-2000; 2000US-234583P.
PR   03-NOV-2000; 2000US-245495P.
PR   31-JUL-2001; 2001US-0919162.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Renauld J,  Dumoutier L;
XX
DR   WPI; 2002-383190/41.
DR   N-PSDB; ABK50076.
XX
PT   Polynucleotide and polypeptide of soluble protein which binds to
PT   interleukin-TIF/IL-22 useful for inhibiting effect of IL-TIF/IL-22 on a
PT   cell  -
XX
PS   Claim 14; Page 39; 42pp; English.
XX
CC   The present invention relates to a new polynucleotide that encodes a
```

CC soluble protein which binds to interleukin (IL)-TIF/IL-22 (also referred
CC to as IL-22BP), where the complementary sequence of the invention
CC hybridises under stringent conditions to a nucleotide sequence of 2271
CC or 2366 base pairs, as given in the specification. The molecules of the
CC invention are useful for inhibiting (antagonising) effect of IL-TIF/IL-22
CC on a cell, for determining whether IL-TIF/IL-22 is present in a sample,
CC for inhibiting binding of IL-TIF/IL-22 to a binding partner, preferably
CC in vitro, and for obtaining an antibody molecule specific for the soluble
CC binding protein of the invention, from a population or panel of antibody
CC molecules of diverse binding specificity. The soluble protein is further
CC useful in manufacture of a medicament for treating an IL-22 mediated
CC disease and for assaying an agent, preferably an antibody or a peptide
CC fragment of IL-TIF/IL-22 or the soluble protein, that modulates binding
CC of the soluble protein to IL-TIF/IL-22, where the agent identified is
CC used in the manufacture of medicament for treating IL-TIF/IL-22 mediated
CC disorder. The antibody is useful for determining presence of the soluble
CC protein, where the antibody is detectably labelled. The present amino
CC acid sequence represents the human IL-TIF/IL-22 binding protein #1 of
CC the invention.

SQ Sequence 231 AA;

Query Match 85.0%; Score 1213; DB 23; Length 231;
Best Local Similarity 87.8%; Pred. No. 5.2e-113;
Matches 230; Conservative 0; Mismatches 0; Indels 32; Gaps 1;

```
Qy       1 MPKHCFLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVYF 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2 MPKHCFLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVYF 61

Qy      61 VQYKIMFSCSMKSSHQKPSGCWQHISCNFPGCRTLAKYGQRQWKNKEDCWGTQELSCDLT 120
           |||||                                ||||||||||||||||||||||
Db      62 VQYKI--------------------------------YGQRQWKNKEDCWGTQELSCDLT 89

Qy     121 SETSDIQEPYYGRVRAASAGSYSEWSMTPRFTPWWETKIDPPVMNITQVNGSLLVILHAP 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      90 SETSDIQEPYYGRVRAASAGSYSEWSMTPRFTPWWETKIDPPVMNITQVNGSLLVILHAP 149

Qy     181 NLPYRYQKEKNVSIEDYYELLYRVFIINNSLEKEQKVYEGAHRAVEIEALTPHSSYCVVA 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     150 NLPYRYQKEKNVSIEDYYELLYRVFIINNSLEKEQKVYEGAHRAVEIEALTPHSSYCVVA 209

Qy     241 EIYQPMLDRRSQRSEERCVEIP 262
           |||||||||||||||||||||||
Db     210 EIYQPMLDRRSQRSEERCVEIP 231
```

RESULT 10
ABG34086
ABG34086 standard; Protein; 231 AA.
XX
AC ABG34086;
XX
DT 15-JUL-2002 (first entry)
XX
DE Human Pro peptide #57.
XX
KW Human; PRO; secreted protein; transmembrane protein;
KW genetic disorder; tumour; cancer.
XX
OS Homo sapiens.
XX
PN WO200224888-A2.
XX
PD 28-MAR-2002.
XX
PF 29-AUG-2001; 2001WO-US27099.
XX
PR 01-SEP-2000; 2000US-229896P.
PR 05-SEP-2000; 2000US-230621P.
PR 22-SEP-2000; 2000US-235147P.
PR 10-NOV-2000; 2000WO-US30873.
PR 12-JAN-2001; 2001US-261878P.
PR 16-JAN-2001; 2001US-261910P.
PR 16-JAN-2001; 2001US-261939P.
PR 16-JAN-2001; 2001US-262150P.
PR 25-JAN-2001; 2001US-264395P.
PR 02-FEB-2001; 2001US-266421P.
PR 09-FEB-2001; 2001US-267623P.
PR 28-FEB-2001; 2001WO-US06520.
PR 09-MAR-2001; 2001US-274399P.
PR 03-APR-2001; 2001US-280982P.
PR 04-APR-2001; 2001US-282129P.
PR 04-APR-2001; 2001US-282199P.
PR 09-MAY-2001; 2001US-290589P.
PR 25-MAY-2001; 2001WO-US17092.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;
PI Gurney AL, Smith V, Stephan J, Watanabe CK, Wood WI, Zhang Z;
PI Fong S;
XX
DR WPI; 2002-362426/39.
DR N-PSDB; ABK70017.
XX
PT New PRO polypeptides and polynucleotides encoding the polypeptides,
PT useful in gene therapy, chromosome identification, tissue typing, or
PT for genetic analysis of individuals with genetic disorders -
XX
PS Claim 11; Figure 114; 218pp; English.
XX
CC This invention relates to the cDNA and protein sequences of novel
CC secreted and transmembrane polypeptides PRO polypeptides. The
CC invention also comprises a method for producing the proteins of the
CC invention by recombinant means and antibodies specific for the protein
CC of the invention. The antibody may be used for detecting the PRO
CC proteins of the invention and may be used to modify their activity.
CC polynucleotides may be used as hybridisation probes for a cDNA library
CC to isolate the full-length PRO cDNA or to isolate other cDNAs, to
CC construct hybridisation probes for mapping the gene which encodes that
CC PRO and for genetic analysis of individuals with genetic disorders, in
CC assays to identify other proteins or molecules involved in binding
CC reaction, to generate transgenic animals or knock-out animals which in
CC turn are useful in the development and screening of therapeutically
CC useful reagents, for chromosome identification, and tissue typing. The
CC PRO polypeptides are useful in gene therapy, and as molecular weight
CC markers for protein electrophoresis purposes. The sequences may
CC also be used to detect overexpression on PRO polypeptides in cancerous
CC tumours and for screening for differentially expressed genes using
CC microarray technology. The present sequence represents a human PRO
CC protein of the invention.
XX
SQ Sequence 231 AA;

Query Match 85.0%; Score 1213; DB 23; Length 231;
Best Local Similarity 87.8%; Pred. No. 5.2e-113;
Matches 230; Conservative 0; Mismatches 0; Indels 32; Gaps 1;

```
Qy       1 MPKHCFLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVYF 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2 MPKHCFLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVYF 61

Qy      61 VQYKIMFSCSMKSSHQKPSGCWQHISCNFPGCRTLAKYGQRQWKNKEDCWGTQELSCDLT 120
           |||||                                ||||||||||||||||||||||
Db      62 VQYKI--------------------------------YGQRQWKNKEDCWGTQELSCDLT 89

Qy     121 SETSDIQEPYYGRVRAASAGSYSEWSMTPRFTPWWETKIDPPVMNITQVNGSLLVILHAP 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      90 SETSDIQEPYYGRVRAASAGSYSEWSMTPRFTPWWETKIDPPVMNITQVNGSLLVILHAP 149

Qy     181 NLPYRYQKEKNVSIEDYYELLYRVFIINNSLEKEQKVYEGAHRAVEIEALTPHSSYCVVA 240
```

```
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    150 NLPYRYQKEKNVSIEDYYELLYRVFIINNSLEKEQKVYEGAHRAVEIEALTPHSSYCVVA 209

Qy    241 EIYQPMLDRRSQRSEERCVEIP 262
          ||||||||||||||||||||||
Db    210 EIYQPMLDRRSQRSEERCVEIP 231
```

RESULT 11
AAE17320
ID AAE17320 standard; Protein; 231 AA.
XX
AC AAE17320;
XX
DT 18-APR-2002 (first entry)
XX
DE Human cytokine receptor protein, sbg456548CytoRa #2.
XX
KW Human; therapy; wound healing disorder; vaccine; cancer; infection;
KW autoimmune disorder; haematopoietic disorder; inflammation; arthritis;
KW Parkinson's disease; Huntington's chorea; schizophrenia; antiarrhythmic;
KW multiple sclerosis; Alzheimer's disease; analgesic; cardiant; asthma;
KW ischaemia; stroke; AIDS; bone disease; atherosclerosis; brain disorder;
KW depression; cardiovascular disease; myocardial infarction; renal failure;
KW respiratory disease; liver disorder; Fanconi's syndrome; spleen disorder;
KW type II diabetes mellitus; skeletal muscle disorder; immunosuppressive;
KW hypersplenism; renal disease; hypoglycaemia; gastrointestinal disease;
KW nootropic; cirrhosis; Hodgkin's disease; neuroleptic; antiinflammatory;
KW haemostatic; vulnerary; anticonvulsant; antirheumatic; neuroprotective;
KW nephrotropic; hypotensive; vasotropic; cytostatic; cerebroprotective;
KW allergy; cytokine receptor.
XX
OS Homo sapiens.
XX
PN WO200198342-A1.
XX
PD 27-DEC-2001.
XX
PF 22-JUN-2001; 2001WO-US19929.
XX
PR 22-JUN-2000; 2000US-213156P.
PR 22-JUN-2000; 2000US-213161P.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PA (GLAX) GLAXO GROUP LTD.
XX
Agarwal P, Cogswell JP, Kabnic KS, Lai Y, Martensen SA;
Murdock PR, Smith RF, Strum JC, Xiang Z, Xie Q, Rizni SK;

DR WPI; 2002-139783/18.
DR N-PSDB; AAD27815.
XX
PT Novel secreted and membrane-associated polypeptides and polynucleotides
PT useful for preventing, ameliorating or correcting dysfunction or
PT disease including diabetes, cancer, hypertension and growth
PT abnormalities -
XX
PS Claim 1; Page 132-133; 138pp; English.
XX
CC The invention relates to secreted and membrane-associated polypeptides
CC and polynucleotides. The sequences of the invention are useful in
CC diagnostic assays for detecting diseases associated with inappropriate
CC activity or levels of these polynucleotides, and in identifying their
CC agonists and antagonists that are potentially useful in therapy. The
CC sequences of the invention are useful as vaccines for inducing
CC immunological response. The sequences of the invention are useful for
CC treating cancers, infections, autoimmune disorders, haematopoietic
CC disorders, wound healing disorders, cholesteryl ester storage disease,
CC inflammation, congenital muscular dystrophy, junctional epidermolysis
CC bullosa, Parkinson's disease, Huntington's chorea, multiple sclerosis,
CC viral and bacterial infections, Alzheimer's disease, asthma, arthritis,
CC allergies, schizophrenia, sbg442445PROa-associated disorders,
CC septicaemia, psoriasis, inflammatory bowel disease, transplant rejection,
CC graft verse host disease, ischaemia, stroke, acute respiratory disease
CC syndrome, restenosis, brain injury, AIDS, bone diseases, atherosclerosis,
CC brain disorders including parasupranuclear palsy, myotonic dystrophy,
CC depression, anxiety disorders and sleep disorders, cardiovascular
CC diseases including congestive heart failure and myocardial infarction,
CC respiratory diseases including chronic obstructive pulmonary disease,
CC acute bronchitis and adult respiratory distress syndrome, liver disorders
CC including hypercholesterolaemia, hypertriglyceridaemia, cirrhosis, viral
CC and non-viral hepatitis, type II diabetes mellitus, renal disease
CC including acute and chronic renal failure, glomerulonephritis, Fanconi's
CC syndrome, cystinuria, skeletal muscle disorders including hypoglycaemia
CC and tendinitis, gastrointestinal diseases including intestinal
CC obstruction and tropical sprue, spleen disorders including hypersplenism,
CC Hodgkin's disease and malignant lymphoma, testicular cancer, male
CC reproductive diseases including low testosterone and male infertility.
CC The present sequence is human cytokine receptor.
XX
SQ Sequence 231 AA;

```
  Query Match             85.0%;  Score 1213;  DB 23;  Length 231;
  Best Local Similarity   87.8%;  Pred. No. 5.2e-113;
  Matches  230;  Conservative    0;  Mismatches    0;  Indels   32;  Gaps    1;

Qy      1 MPKHCFLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVYF 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2 MPKHCFLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVYF 61

Qy     61 VQYKIMFSCSMKSSHQKPSGCWQHISCNFPGCRTLAKYGQRQWKNKEDCWGTQELSCDLT 120
          |||||                              ||||||||||||||||||||||||
Db     62 VQYKI------------------------------YGQRQWKNKEDCWGTQELSCDLT 89

Qy    121 SETSDIQEPYYGRVRAASAGSYSEWSMTPRFTPWWETKIDPPVMNITQVNGSLLVILHAP 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     90 SETSDIQEPYYGRVRAASAGSYSEWSMTPRFTPWWETKIDPPVMNITQVNGSLLVILHAP 149

Qy    181 NLPYRYQKEKNVSIEDYYELLYRVFIINNSLEKEQKVYEGAHRAVEIEALTPHSSYCVVA 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    150 NLPYRYQKEKNVSIEDYYELLYRVFIINNSLEKEQKVYEGAHRAVEIEALTPHSSYCVVA 209

Qy    241 EIYQPMLDRRSQRSEERCVEIP 262
          ||||||||||||||||||||||
Db    210 EIYQPMLDRRSQRSEERCVEIP 231
```

RESULT 12
AAE17319
ID AAE17319 standard; Protein; 214 AA.
XX
AC AAE17319;
XX
DT 18-APR-2002 (first entry)
XX
DE Human cytokine receptor protein, sbg456548CytoRa #1.
XX
KW Human; therapy; wound healing disorder; vaccine; cancer; infection;
KW autoimmune disorder; haematopoietic disorder; inflammation; arthritis;
KW Parkinson's disease; Huntington's chorea; schizophrenia; antiarrhythmic;
KW multiple sclerosis; Alzheimer's disease; analgesic; cardiant; asthma;
KW ischaemia; stroke; AIDS; bone disease; atherosclerosis; brain disorder;
KW depression; cardiovascular disease; myocardial infarction; renal failure;
KW respiratory disease; liver disorder; Fanconi's syndrome; spleen disorder;
KW type II diabetes mellitus; skeletal muscle disorder; immunosuppressive;
KW hypersplenism; renal disease; hypoglycaemia; gastrointestinal disease;
KW nootropic; cirrhosis; Hodgkin's disease; neuroleptic; antiinflammatory;
KW haemostatic; vulnerary; anticonvulsant; antirheumatic; neuroprotective;
KW nephrotropic; hypotensive; vasotropic; cytostatic; cerebroprotective;
KW allergy; cytokine receptor.
XX
OS Homo sapiens.
XX
PN WO200198342-A1.
XX

PD 27-DEC-2001.
XX
PF 22-JUN-2001; 2001WO-US19929.
XX
PR 22-JUN-2000; 2000US-213156P.
PR 22-JUN-2000; 2000US-213161P.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PA (GLAX) GLAXO GROUP LTD.
XX
PI Agarwal P, Cogswell JP, Kabnic KS, Lai Y, Martensen SA;
PI Murdock PR, Smith RF, Strum JC, Xiang Z, Xie Q, Rizni SK;
XX
DR WPI; 2002-139783/18.
DR N-PSDB; AAD27814.
XX
PT Novel secreted and membrane-associated polypeptides and polynucleotides
PT useful for preventing, ameliorating or correcting dysfunction or
PT disease including diabetes, cancer, hypertension and growth
PT abnormalities -
XX
PS Claim 1; Page 122; 138pp; English.
XX
CC The invention relates to secreted and membrane-associated polypeptides
CC and polynucleotides. The sequences of the invention are useful in
CC diagnostic assays for detecting diseases associated with inappropriate
CC activity or levels of these polynucleotides, and in identifying their
CC agonists and antagonists that are potentially useful in therapy. The
CC sequences of the invention are useful as vaccines for inducing
CC immunological response. The sequences of the invention are useful for
CC treating cancers, infections, autoimmune disorders, haematopoietic
CC disorders, wound healing disorders, cholesteryl ester storage disease,
CC inflammation, congenital muscular dystrophy, junctional epidermolysis
CC bullosa, Parkinson's disease, Huntington's chorea, multiple sclerosis,
CC viral and bacterial infections, Alzheimer's disease, asthma, arthritis,
CC allergies, schizophrenia, sbg442445PROa-associated disorders,
CC septicaemia, psoriasis, inflammatory bowel disease, transplant rejection,
CC graft verse host disease, ischaemia, stroke, acute respiratory disease
CC syndrome, restenosis, brain injury, AIDS, bone diseases, atherosclerosis,
CC brain disorders including parasupranuclear palsy, myotonic dystrophy,
CC depression, anxiety disorders and sleep disorders, cardiovascular
CC diseases including congestive heart failure and myocardial infarction,
CC respiratory diseases including chronic obstructive pulmonary disease,
CC acute bronchitis and adult respiratory distress syndrome, liver disorders
CC including hypercholesterolaemia, hypertriglyceridaemia, cirrhosis, viral
CC and non-viral hepatitis, type II diabetes mellitus, renal disease
CC including acute and chronic renal failure, glomerulonephritis, Fanconi's
CC syndrome, cystinuria, skeletal muscle disorders including hypoglycaemia
CC and tendinitis, gastrointestinal diseases including intestinal
CC obstruction and tropical sprue, spleen disorders including hypersplenism,
CC Hodgkin's disease and malignant lymphoma, testicular cancer, male
CC reproductive diseases including low testosterone and male infertility.
CC The present sequence is human cytokine receptor.
XX
SQ Sequence 214 AA;

Query Match 78.1%; Score 1114; DB 23; Length 214;
Best Local Similarity 86.9%; Pred. No. 3.8e-103;
Matches 212; Conservative 0; Mismatches 0; Indels 32; Gaps 1;

```
Qy      19 AGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVYFVQYKIMFSCSMKSSHQKP 78
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3 AGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVYFVQYKI---------- 49

Qy      79 SGCWQHISCNFPGCRTLAKYGQRQWKNKEDCWGTQELSCDLTSETSDIQEPYYGRVRAAS 138
                          ||||||||||||||||||||||||||||||||||||||||||||
Db      50 ------------------YGQRQWKNKEDCWGTQELSCDLTSETSDIQEPYYGRVRAAS 90

Qy     139 AGSYSEWSMTPRFTPWWETKIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYY 198
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      91 AGSYSEWSMTPRFTPWWETKIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYY 150

Qy     199 ELLYRVFIINNSLEKEQKVYEGAHRAVEIEALTPHSSYCVVAEIYQPMLDRRSQRSEERC 258
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     151 ELLYRVFIINNSLEKEQKVYEGAHRAVEIEALTPHSSYCVVAEIYQPMLDRRSQRSEERC 210

Qy     259 VEIP 262
           ||||
Db     211 VEIP 214
```

RESULT 13
AAB62663
ID AAB62663 standard; Protein; 210 AA.
XX
AC AAB62663;
XX
DT 23-JUL-2001 (first entry)
XX
DE Human zcytor16 extracellular domain fragment (residues 22-231).
XX
KW Cytokine receptor; zcytor16; IL-TIF; antiinflammatory; cytostatic;
KW antirheumatic; antiarthritic; antiasthmatic; antiatherosclerotic;
KW immunosuppressive; chromosome 6q24.1-25.2; human.
XX
OS Homo sapiens.
XX
PN WO200140467-A1.
XX
PD 07-JUN-2001.
XX
PF 01-DEC-2000; 2000WO-US32703.
XX
PR 03-DEC-1999; 99US-0169049.
PR 13-SEP-2000; 2000US-0232219.
PR 31-OCT-2000; 2000US-0244610.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Presnell SR, Xu W, Kindsvogel W, Chen Z;
XX
DR WPI; 2001-356158/37.
XX
PT New soluble cytokine receptor polypeptides and polynucleotides, useful
PT for diagnosing and treating cancer and inflammatory conditions -
XX
PS Claim 1; Page 193; 210pp; English.
XX
CC The invention relates to a human cytokine receptor polypeptide,
CC designated zcytor16. The zcytor16 polypeptide can be expressed by
CC standard recombinant methodology and can bind to IL-TIF (undefined). The
CC zcytor16 protein is useful for: inhibiting IL-TIF induced proliferation
CC or differentiation of hematopoietic cell(s) (progenitors); reducing
CC IL-TIF induced or IL-9 induced inflammation; and suppressing an
CC inflammatory response in a mammal with inflammation. Heteromeric/
CC multimeric receptor polypeptides such as soluble zcytor 16/CRF2-4 can be
CC used to reduce progression and symptoms of cancer. Zcytor16 polypeptides
CC can also be used to detect IL-TIF levels which is indicative of
CC pathological conditions including inflammatory states (e.g. rheumatoid
CC arthritis) and cancer. Antibodies that bind zcytor16 polypeptides and the
CC polypeptides themselves are useful for the treatment of inflammation,
CC inflammatory diseases (e.g. infection, asthma, inflammatory bowel
CC disease, rheumatoid arthritis and atherosclerosis) and autoimmune
CC diseases. The antibodies and zcytor16 polynucleotides are also useful
CC for detecting cancer. The present sequence represents the human zcytor16
CC extracellular domain fragment.
XX
SQ Sequence 210 AA;

Query Match 77.4%; Score 1104; DB 22; Length 210;
Best Local Similarity 86.8%; Pred. No. 3.7e-102;
Matches 210; Conservative 0; Mismatches 0; Indels 32; Gaps 1;

```
Qy      21 TQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVYFVQYKIMFSCSMKSSHQKPSG 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db       1 TQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVYFVQYKI--------------- 45

Qy      81 CWQHISCNFPGCRTLAKYGQRQWKNKEDCWGTQELSCDLTSETSDIQEPYYGRVRAASAG 140
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      46 -----------------YGQRQWKNKEDCWGTQELSCDLTSETSDIQEPYYGRVRAASAG 88

Qy     141 SYSEWSMTPRFTPWWETKIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYYEL 200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      89 SYSEWSMTPRFTPWWETKIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYYEL 148

Qy     201 LYRVFIINNSLEKEQKVYEGAHRAVEIEALTPHSSYCVVAEIYQPMLDRRSQRSEERCVE 260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     149 LYRVFIINNSLEKEQKVYEGAHRAVEIEALTPHSSYCVVAEIYQPMLDRRSQRSEERCVE 208

Qy     261 IP 262
           ||
Db     209 IP 210
```

[redacted]ULT 14
[redacted]2458
ID AAE02458 standard; Protein; 249 AA.
XX
AC AAE02458;
XX
DT 10-AUG-2001 (first entry)
XX
DE Human DNAX cytokine receptor subunit 4.1 (DCRS4.1).
XX
KW Human; immunomodulator; DNAX cytokine receptor subunit 4.1; DCRS4.1;
KW therapy; immunological disorder; drug screening; cell development;
KW chromosome 6q24.1-25.2.
XX
OS Homo sapiens.
XX

FH	Key	Location/Qualifiers
FT	Peptide	1..21
FT		/label= Signal-peptide
FT	Protein	22..249
FT		/label= DCRS4.1
FT		/note= "Human mature DNAX cytokine receptor
FT		subunit 4.1"
FT	Modified-site	24
FT		/note= "CK2 phosphorylation site"
FT	Modified-site	25
FT		/note= "Calcium phosphorylation site"
FT	Modified-site	28
FT		/note= "PKC phosphorylation site"
[redacted]	Domain	31..70
FT		/label= Cytokine_receptor_domain
FT	Modified-site	51
FT		/note= "cAMP PK site"
FT	Modified-site	56
FT		/note= "N-glycosylated"
FT	Disulfide-bond	78..86
FT		/label= Conserved_disulphide_linkage
FT	Modified-site	81
FT		/note= "Calcium phosphorylation site"
FT	Modified-site	85
FT		/note= "Calcium phosphorylation site"
FT	Modified-site	89
FT		/note= "Calcium phosphorylation site"
FT	Modified-site	92
FT		/note= "Calcium phosphorylation site"
FT	Modified-site	100
FT		/note= "Amidation site"
FT	Modified-site	110
FT		/note= "Myristoyl site"
FT	Modified-site	118
FT		/note= "PKC phosphorylation site"
FT	Modified-site	119
FT		/note= "cAMP phosphorylation site"
FT	Modified-site	119
FT		/note= "cAMP PK site"
FT	Modified-site	124
FT		/note= "Myristoyl site"
FT	Modified-site	127
FT		/note= "cAMP PK site"
FT	Modified-site	152
FT		/note= "N-glycosylated"
FT	Modified-site	157
FT		/note= "N-glycosylated"
FT	Modified-site	177
FT		/note= "cAMP PK site"
FT	Modified-site	178
FT		/note= "N-glycosylated"
FT	Modified-site	180
FT		/note= "Calcium phosphorylation site"
FT	Modified-site	180
FT		/note= "CK2 phosphorylation site"
FT	Modified-site	195
FT		/note= "N-glycosylated"
FT	Modified-site	197
FT		/note= "Calcium phosphorylation site"
FT	Modified-site	207
FT		/note= "Myristoyl site"
FT	Modified-site	238
FT		/note= "PKC phosphorylation site"
FT	Modified-site	241
FT		/note= "Calcium phosphorylation site"

XX
PN WO200136467-A2.
XX
PD 25-MAY-2001.
XX
PF 16-NOV-2000; 2000WO-US31363.
XX
PR 18-NOV-1999; 99US-0443060.
PR 13-DEC-1999; 99US-0170320.
XX
PA (SCHE) SCHERING CORP.
XX
PI Gorman DM;
XX
DR WPI; 2001-343800/36.
DR N-PSDB; AAD06410.
XX
PT New mammalian receptor proteins related to cytokine receptors, useful
PT for regulating cell development and for diagnosis and treatment of
PT immunological disorders -
XX
PS Claim 3; Page 22; 124pp; English.
XX
CC The present sequence is human DNAX cytokine receptor subunit 4.1
CC (DCRS4.1). DCRS4 gene is located on chromosome 6q24.1-25.2.
CC Cytokine receptors, fragments and antibodies are useful for treating
CC immunological disorders. DCRS3 (50R), DCRS4 (cytor) or fragments are
CC useful in drug screening to identify compounds having binding affinity
CC to the receptor subunit. Modulators of DCRS are useful for modulating
CC the physiology or development of a cell or tissue culture cells. A
CC purified DCRS is useful as a reagent to detect antibodies generated in
CC response to the presence of elevated levels of expression, or
CC immunological disorders which lead to production of antibody to the
CC endogenous receptor. Cytokine receptor sequences are useful as probes
CC for detecting levels of the cytokine receptor in patients suspected of
CC having an immunological disorder. Antibodies have therapeutic value, are
CC useful as potent antagonist, in detecting or quantifying ligands, for
CC isolating DCRS proteins and peptides, to screen expression libraries for
CC particular expression products, to raise anti-idiotypic antibodies and
CC for detecting or diagnosing various immunological conditions related to
CC expression of the protein or cells which express the protein.
XX
SQ Sequence 249 AA;

Query Match	73.2%;	Score 1045;	DB 22; Length 249;
Best Local Similarity	74.4%;	Pred. No. 3.8e-96;	

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  Matches  209;  Conservative    3;  Mismatches   17;  Indels   52;  Gaps    4;

Qy       1 MPKHCFLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVYF 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2 MPKHCFLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVYF 61

Qy      61 VQYKIMFSCSMKSSHQKPSGCWQHISCNFPGCRTLAKYGQRQWKNKEDCWGTQELSCDLT 120
           |||||                            |||||||||||||||||||||||
Db      62 VQYKI------------------------------YGQRQWKNKEDCWGTQELSCDLT 89

Qy     121 SETSDIQEPYYGRVRAASAGSYSEWS----------------MTPRFTPWWE--TKIDP 161
           |||||||||||||  |  :    : |                  |     :    ||||
Db      90 SETSDIQEPYYGR-RGKNKNKGNPWGPKQSKRKSKGNQKTNTVTAPAALKAFAGCAKIDP 148

Qy     162 PVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYYELLYRVFIINNSLEKEQKVYEGA 221
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     149 PVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYYELLYRVFIINNSLEKEQKVYEGA 208

Qy     222 HRAVEIEALTPHSSYCVVAEIYQPMLDRRSQRSEERCVEIP 262
           |||||||||||||||||||||||||||||||||||||||||
Db     209 HRAVEIEALTPHSSYCVVAEIYQPMLDRRSQRSEERCVEIP 249


RESULT 15
AAO17380
ID   AAO17380 standard; Protein; 249 AA.
XX
AC   AAO17380;
XX
DT   08-AUG-2002  (first entry)
XX
DE   Human cytokine receptor variant 1.
XX
KW   Human; cytokine receptor; immune disease; psoriasis; cancer; infection;
KW   rheumatoid arthritis; multiple sclerosis; Crohn's disease;
KW   ulcerative colitis; transplant rejection; abortion; antipsoriatic;
KW   immunosuppressive; antirheumatic; antiarthritic; neuroprotective;
KW   antiinflammatory; antiulcer; cytostatic; dermatological;
KW   chromosome 6q24.1-25.2; receptor.
XX
OS   Homo sapiens.
XX
PN   EP1191035-A2.
XX
PD   27-MAR-2002.
XX
PF   24-AUG-2001; 2001EP-0250307.
XX
PR   25-SEP-2000; 2000DE-1048626.
PR   17-NOV-2000; 2000DE-1058907.
PR   19-DEC-2000; 2000DE-1064906.
XX
PA   (SCHD ) SCHERING AG.
XX
PI   Weiss B,  Sabat R,  Assadullah K,  Toshi L;
XX
DR   WPI; 2002-332210/37.
DR   N-PSDB; AAL45999.
XX
PT   New nucleic acid encoding soluble cytokine receptor, useful for
PT   diagnosis and treatment of e.g. immune disease, also related protein
PT   and antibodies  -
XX
PS   Claim 6; Page 12-13; 21pp; German.
XX
CC   The present invention provides the protein and coding sequences of 3
CC   variants of a human cytokine receptor. The sequences can be used in the
CC   diagnosis, prevention and treatment of immune diseases, including
CC   psoriasis, cancer, chronic/life-threatening infections, rheumatoid
CC   arthritis, multiple sclerosis, Crohn's disease, ulcerative colitis and
CC   transplant rejection and in reproductive medicine, e.g. for diagnosing
CC   abnormal immune reactions which cause abortions. The present sequence is
CC   variant 1 of the invention.
XX
SQ   Sequence   249 AA;

  Query Match             73.2%;  Score 1045;  DB 23;  Length 249;
  Best Local Similarity   74.4%;  Pred. No. 3.8e-96;
  Matches  209;  Conservative    3;  Mismatches   17;  Indels   52;  Gaps    4;

Qy       1 MPKHCFLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVYF 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2 MPKHCFLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVYF 61

Qy      61 VQYKIMFSCSMKSSHQKPSGCWQHISCNFPGCRTLAKYGQRQWKNKEDCWGTQELSCDLT 120
           |||||                            |||||||||||||||||||||||
Db      62 VQYKI------------------------------YGQRQWKNKEDCWGTQELSCDLT 89

Qy     121 SETSDIQEPYYGRVRAASAGSYSEWS----------------MTPRFTPWWE--TKIDP 161
           |||||||||||||  |  :    : |                  |     :    ||||
Db      90 SETSDIQEPYYGR-RGKNKNKGNPWGPKQSKRKSKGNQKTNTVTAPAALKAFAGCAKIDP 148

Qy     162 PVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYYELLYRVFIINNSLEKEQKVYEGA 221
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     149 PVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYYELLYRVFIINNSLEKEQKVYEGA 208

Qy     222 HRAVEIEALTPHSSYCVVAEIYQPMLDRRSQRSEERCVEIP 262
           |||||||||||||||||||||||||||||||||||||||||
Db     209 HRAVEIEALTPHSSYCVVAEIYQPMLDRRSQRSEERCVEIP 249


Search completed: December 22, 2002, 10:10:49
Job time : 68 secs
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GenCore version 5.1.3

OM protein - protein search, using sw model

Run on: December 22, 2002, 10:08:17 ; Search time 44 Seconds
(without alignments)
572.437 Million cell updates/sec

Title: US-09-964-994-2
Perfect score: 1427
Sequence: 1 MPKHCFLGFLISFFLTGVAG.....YQPMLDRRSQRSEERCVEIP 262

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

[redacted]l number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	164.5	11.5	575	2	A49667	interleukin-10 rec
2	163	11.4	295	1	KFHU3	tissue factor prec
3	158	11.1	560	2	S27387	interferon alpha r
4	156	10.9	349	2	JC6311	interferon recepto
5	152.5	10.7	578	2	I56215	interleukin-10 rec
6	149.5	10.5	325	2	A47003	cytokine receptor
7	138.5	9.7	292	1	KFBO3	tissue factor prec
8	136.5	9.6	557	2	A32694	interferon alpha/b
9	134.5	9.4	590	2	A45283	interferon alpha/b
10	132.5	9.3	292	1	KFRB3	tissue factor prec
11	122.5	8.6	489	2	A31555	interferon gamma r
12	122	8.5	294	1	KFMS3	tissue factor prec
13	110.5	7.7	332	2	A49947	interferon gamma r
14	103.5	7.3	515	2	I39073	interferon alpha-b
15	101.5	7.1	331	2	A54295	interferon alpha/b
16	101.5	7.1	331	2	S59501	interferon recepto
17	92	6.4	337	2	I38500	interferon gamma r
18	90	6.3	1253	1	VHWV	structural polypro
19	88	6.2	755	2	S42462	structural polypro
20	87.5	6.1	674	2	A47222	Kallmann syndrome
21	87.5	6.1	676	2	B47222	Kallmann syndrome
22	87	6.1	1145	2	S37136	structural polypro
23	87	6.1	1384	2	T02748	hypothetical prote
24	86	6.0	477	2	A34368	interferon gamma r
25	85	6.0	792	2	S16680	ribonucleoside-dip
26	85	6.0	810	2	E71550	probable phospholi
27	84.5	5.9	703	2	T41065	RNA binding protei
28	84.5	5.9	1059	2	T13928	probable transcrip
29	84.5	5.9	1083	2	T13929	probable transcrip
30	83	5.8	266	2	I36855	gene B9R protein -
31	83	5.8	479	2	T02623	hypothetical prote
32	82.5	5.8	478	1	LEECD	hemolysin export s
33	82.5	5.8	650	2	T15972	hypothetical prote
34	81.5	5.7	456	2	B86834	sensor protein kin
35	81	5.7	430	2	T25489	hypothetical prote
36	81	5.7	564	2	T21423	hypothetical prote
37	81	5.7	810	1	S57196	calpain (EC 3.4.22
38	81	5.7	1247	1	VHWVN2	structural polypro
39	80.5	5.6	478	2	S10058	hemolysin secretio
40	80.5	5.6	527	2	T02128	beta-glucosidase h
41	80	5.6	426	2	JC7773	IL-13Ralpha 1 prot
42	80	5.6	582	2	A32034	choline kinase (EC
43	80	5.6	884	2	T01041	hypothetical prote
44	79.5	5.6	1266	2	AF0911	probable exported
45	79	5.5	335	2	AG2311	hypothetical prote

ALIGNMENTS

RESULT 1
A49667
interleukin-10 receptor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 28-Jul-2000
C;Accession: A49667
R;Ho, A.S.; Liu, Y.; Khan, T.A.; Hsu, D.H.; Bazan, J.F.; Moore, K.W.
Proc. Natl. Acad. Sci. U.S.A. 90, 11267-11271, 1993
A;Title: A receptor for interleukin 10 is related to interferon receptors.
A;Reference number: A49667; MUID:94068585; PMID:8248239
A;Accession: A49667
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-575 <RES>
A;Cross-references: GB:L12120; NID:g437615; PIDN:AAA16156.1; PID:g437616
C;Genetics:
A;Gene: Il10r
C;Superfamily: interleukin-10 receptor IL10R
C;Keywords: cytokine receptor

Query Match 11.5%; Score 164.5; DB 2; Length 575;
Best Local Similarity 26.7%; Pred. No. 1.4e-06;
Matches 74; Conservative 37; Mismatches 89; Indels 77; Gaps 16;

```
Qy       6 FLGFLISFFLTGVA-GTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVYFVQYK 64
           ||  : |  |  :| ||    |   |  | |::| | :|| |:|     : | |   |:
Db       8 FLVTISSLSLEFIAYGT----ELPSPSYVWFEARFFQHILHWKP--IPNQSESTY---YE 58

Qy      65 IMFSCSMKSSHQKPSGCWQHISCNFPGCRTLAKYGQRQWKNKEDCWGTQELSCDLTSETS 124
           :                            | :||   | :   |   | |||||| : |
Db      59 V----------------------------ALKQYGNSTWNDIHICRKAQALSCDLTTFTL 90

Qy     125 DIQEPYYG---RVRAASAGSYSEWSMT-PRFTPWWETKIDPPVMNITQV-----NGSLLV 175
           |:    ||   ||||     || |: |  |||      :|  :: :  |     :| :
Db      91 DLYHRSYGYRARVRAVDNSQYSNWTTTETRFT------VDEVILTVDSVTLKAMDGIIYG 144

Qy     176 ILHAPNLPYRYQKEKNVSIEDYYELLY---RVFIINNSLEKEQKVYEGAHRAVEIEALT- 231
            :| |       :       | || ::   ||: |  |: |  :: : | : |: |  |
Db     145 TIHPP-------RPTITPAGDEYEQVFKDLRVYKI--SIRKFSEL-KNATKRVKQETFTL 194

Qy     232 ----PHSSYCVVAEIYQPMLDRR---SQRSEERCVEI 261
                 :||      | |: |   ::  |||:|: |
Db     195 TVPIGVRKFCVKV---LPRLESRINKAEWSEEQCLLI 228
```

RESULT 2
KFHU3
tissue factor precursor [validated] - human
N;Alternate names: coagulation factor III
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 08-Dec-2000
C;Accession: A43645; A47574; A28320; A29062; A29672; A29008

R;Mackman, N.; Morrissey, J.H.; Fowler, B.; Edgington, T.S.
Biochemistry 28, 1755-1762, 1989
A;Title: Complete sequence of the human tissue factor gene, a highly regulated cellular
A;Reference number: A43645; MUID:89247359; PMID:2719931
A;Accession: A43645
A;Molecule type: DNA
A;Residues: 1-295 <MAC>
A;Cross-references: GB:J02846; NID:g339505; PIDN:AAA61152.1; PID:g339506
R;Fisher, K.L.; Gorman, C.M.; Vehar, G.A.; O'Brien, D.P.; Lawn, R.M.
Thromb. Res. 48, 89-99, 1987
A;Title: Cloning and expression of human tissue factor cDNA.
A;Reference number: A47574; MUID:88100453; PMID:3424286
A;Accession: A47574
A;Molecule type: mRNA
A;Residues: 1-295 <FIS>
A;Cross-references: GB:M27436; NID:g339507; PIDN:AAA36734.1; PID:g339508
R;Spicer, E.K.; Horton, R.; Bloem, L.; Bach, R.; Williams, K.R.; Guha, A.; Kraus, J.; Li
Proc. Natl. Acad. Sci. U.S.A. 84, 5148-5152, 1987
A;Title: Isolation of cDNA clones coding for human tissue factor: primary structure of t
A;Reference number: A94171; MUID:87260946; PMID:3037536
A;Accession: A28320
A;Molecule type: mRNA
A;Residues: 1-295 <SPI>
A;Cross-references: GB:J02931; NID:g339501; PIDN:AAA61150.1; PID:g339502
R;Morrissey, J.H.; Fakhrai, H.; Edgington, T.S.
Cell 50, 129-135, 1987
A;Title: Molecular cloning of the cDNA for tissue factor, the cellular receptor for the
A;Reference number: A29062; MUID:87244317; PMID:3297348
A;Accession: A29062
A;Molecule type: mRNA
A;Residues: 1-295 <MOR>
A;Cross-references: GB:J02931; NID:g339501; PIDN:AAA61150.1; PID:g339502
A;Note: part of this sequence, including the amino end of the mature protein, was confir
R;Scarpati, E.M.; Wen, D.; Broze Jr., G.J.; Miletich, J.P.; Flandermeyer, R.R.; Siegel,
Biochemistry 26, 5234-5238, 1987
A;Title: Human tissue factor: cDNA sequence and chromosome localization of the gene.
A;Reference number: A29672; MUID:88050796; PMID:2823875
A;Accession: A29672
A;Molecule type: mRNA
A;Residues: 1-259,'A',261-295 <SCA>
A;Cross-references: GB:M16553; NID:g339503; PIDN:AAA61151.1; PID:g339504
R;Bach, R.; Konigsberg, W.H.; Nemerson, Y.
Biochemistry 27, 4227-4231, 1988
A;Title: Human tissue factor contains thioester-linked palmitate and stearate on the cyt
A;Reference number: A37422; MUID:89000604; PMID:3166978
A;Contents: annotation; disulfide bonds and fatty acid binding site
C;Comment: Tissue factor is an integral membrane glycoprotein that serves as a receptor
C;Comment: Expression of tissue factor can be induced in a variety of tissues by certain
C;Genetics:
A;Gene: GDB:F3
A;Cross-references: GDB:119895; OMIM:134390
A;Map position: 1p22-1p21
A;Introns: 34/1; 71/2; 138/1; 197/3; 251/1
C;Superfamily: tissue factor
C;Keywords: blood coagulation; glycoprotein; lipoprotein; thiolester bond; transmembrane
F;1-32/Domain: signal sequence #status predicted <SIG>
F;33-295/Product: tissue factor #status experimental <MAT>
F;33-251/Domain: extracellular #status predicted <EXT>
F;252-274/Domain: transmembrane #status predicted <TMM>
F;275-295/Domain: intracellular #status predicted <INT>
F;43/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;81-89,218-241/Disulfide bonds: #status experimental
F;156,169/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;277/Binding site: palmitate (Cys) (covalent) #status experimental

Query Match 11.4%; Score 163; DB 1; Length 295;
Best Local Similarity 23.4%; Pred. No. 7.9e-07;
Matches 62; Conservative 45; Mismatches 100; Indels 58; Gaps 13;

```
Qy      10 LISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVYFVQYKIMFSC 69
           |: :    |||   |  ::    : ::| ||  ||:|:|       : || ||
Db      21 LLGWVFAQVAGASGTTNTVAAYNLTWKSTNFKTILEWEPKPV----NQVYTVQ------I 70
```

```
Qy      70 SMKSSHQKPSGCWQHISCNFPGCRTLAKYGQRQWKNKEDCWGTQELSCDLTSE-TSDIQE 128
           | ||                                ||:|  |: | :  |||| |   |:::
Db      71 STKSG-------------------------DWKSK--CFYTTDTECDLTDEIVKDVKQ 101

Qy     129 PYYGRV------RAASAGSYSE--WSMTPRFTPWWETKI-DPPVMNITQVNGSLLVILHA 179
           |  ||         | ||  |  :  :| |||: || :  | : :  ||   : | :
Db     102 TYLARVFSYPAGNVESTGSAGEPLYENSPEFTPYLETNLGQPTIQSFEQVGTKVNVTVED 161

Qy     180 PNLPYRYQKEKNVSIEDYY--ELLYRVFIINNSLEKEQKVYEGAHR-AVEIEALTPHSSY 236
           |  :   :|: | :  :|:| ::   :|   ::      :   ::::     :|
Db     162 ERTLVR-RNNTFLSLRDVFGKDLIYTLYYWKSSSSGKKTAKTNTNEFLIDVD---KGENY 217

Qy     237 C--VVAEIYQPMLDRRSQRSEERCV 259
           |  | | |    ::|:|  |   |:
Db     218 CFSVQAVIPSRTVNRKSTDSPVECM 242
```

RESULT 3
S27387
interferon alpha receptor type 1 precursor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C;Accession: S27387; S33770
R;Mouchel-Vielh, E.; Lutfalla, G.; Mogensen, K.E.; Uze, G.
FEBS Lett. 313, 255-259, 1992
A;Title: Specific antiviral activities of the human alpha interferons are determined
A;Reference number: S27387; MUID:93076908; PMID:1446745
A;Accession: S27387
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-560 <MOU>
A;Cross-references: EMBL:X68443; NID:g431; PIDN:CAA48484.1; PID:g432
A;Experimental source: MDBK cells
R;Lim, J.K.; Langer, J.A.
Biochim. Biophys. Acta 1173, 314-319, 1993
A;Title: Cloning and characterization of a bovine alpha interferon receptor.
A;Reference number: S33770; MUID:93305725; PMID:8318540
A;Accession: S33770
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-421,'V',423-560 <LIM>
A;Cross-references: EMBL:L06320; NID:g163187; PIDN:AAA02571.1; PID:g163188
A;Experimental source: lung
C;Keywords: antiviral; cytokine receptor; transmembrane protein
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-560/Product: interferon alpha receptor type 1 #status predicted <MAT>

Query Match 11.1%; Score 158; DB 2; Length 560;
Best Local Similarity 24.1%; Pred. No. 5e-06;
Matches 57; Conservative 38; Mismatches 100; Indels 42; Gaps 8;

```
Qy      21 TQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVYFVQYKIMFSCSMKSSHQKPSG 80
           |   |:   |: :|  : |   :|:|         :: :  |:   |   :  :|
Db     223 TTERHKVPSPENIQINADNQIYVLKWD----YPYENATFQAQWLRAFFKKIPGNHSD--- 275

Qy      81 CWQHISCNFPGCRTLAKYGQRQWKNKEDCWGTQELSCDLTSETSDIQEPYYGRVRAASAG 140
                              :||   :|      |    | |  :  || ||||::
Db     276 --------------------KWKQIPNCENVTSTHCVFPREVSS-RGIYYVRVRASNGN 313

Qy     141 SYSEWSMTPRFTPWWETKIDPPVMNITQV-NGSLLVILHAPNLPYRYQKEKNVSIEDYYE 199
           | ||    |    :| | |||:::  | : || | : |       :: :|:|:   |
Db     314 GTSFWSEEKEFNTEMKTIIFPPVISVKSVTDDSLHVSVGAS------EESENMSVNQLYP 367

Qy     200 LLYRVFIINNSLEKEQKVYEGAHRAVEIEALTPHSSYCVVAEIYQPML--DRRSQRS 254
           |:| |    |:   |:|| |     :    | | : ||| |   : ::  |||:: |
Db     368 LIYEVIFWENTSNAERKVLEKRTNFI-FPDLKPLTVYCVKA---RALIENDRRNKGS 420
```

RESULT 4
JC6311
interferon receptor-class II cytokine receptor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 11-May-2000

```
C;Accession: JC6311
R;Gibbs, V.C.; Pennica, D.
Gene 186, 97-101, 1997
A;Title: CRF2-4:isolation of cDNA clones encoding the human and mouse proteins.
A;Reference number: JC6311; MUID:97199375; PMID:9047351
A;Accession: JC6311
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-349 <GIB>
A;Cross-references: GB:U53696

  Query Match            10.9%;  Score 156;  DB 2;  Length 349;
  Best Local Similarity  26.8%;  Pred. No. 4.1e-06;
  Matches   72;  Conservative   30;  Mismatches   89;  Indels   78;  Gaps   13;

Qy       5 CFLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQ----PGRALTGNSSVYF 60
Db       4 CVAGWLGGFLLVPALGMIP-----PPEKVRMNSVNFKNILQWEVPAFPKTNLT-----FT 53

Qy      61 VQYKIMFS----CSMKSSHQKPSGCWQHISCNFPGCRTLAKYGQRQWKNKEDCWGTQELS 116
Db      54 AQYESYRSFQDHCKRTASTQ----------CDF---SHLSKYGD---------------- 84

Qy     117 CDLTSETSDIQEPYYGRVRAASAGSYSEWSMTPRFTPWWETKIDPPVMNITQVNGSLLVI 176
Db      85 ------------YTVRVRAELADEHSEW-VNVTFCPVEDTIIGPPEMQIESLAESLELR 130

Qy     177 LHAPNLPYRYQKE------KNVSIEDYYELLYRV-FIINNSLEKEQKVYEGAHRAVEIEA 229
Db     131 FSAPQI----ENEPETWTLKNI----YDSWAYRVQYWKNGTNEKFQVV--SPYDSEVLRN 180

Qy     230 LTPHSSYCVVAEIYQPMLDRRSQRSEERC 258
Db     181 LEPWTTYCIQVQGFLLDQNRTGEWSEPIC 209


RESULT 5
I56215
interleukin-10 receptor - human
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 28-Jul-2000
C;Accession: I56215
R;Liu, Y.; Wei, S.H.; Ho, A.S.; de Waal Malefyt, R.; Moore, K.W.
J. Immunol. 152, 1821-1829, 1994
A;Title: Expression cloning and characterization of a human IL-10 receptor.
A;Reference number: I56215; MUID:94165477; PMID:8120391
A;Accession: I56215
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-578 <RES>
A;Cross-references: EMBL:U00672; NID:g482802; PIDN:AAA17896.1; PID:g482803
C;Genetics:
A;Gene: GDB:IL10R; HIL-10R
A;Cross-references: GDB:330958; OMIM:146933
A;Map position: 11q23.3-11q23.3
C;Superfamily: interleukin-10 receptor IL10R
C;Keywords: cytokine receptor

  Query Match            10.7%;  Score 152.5;  DB 2;  Length 578;
  Best Local Similarity  24.5%;  Pred. No. 1.6e-05;
  Matches   67;  Conservative   39;  Mismatches   94;  Indels   73;  Gaps   14;

Qy       7 LGFLISFFLTGVA-GTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVYFVQYKI 65
Db       9 LAALLSLRLGSDAHGT----ELPSPPSVWFEAEFFHHILHWTP---------------- 47

Qy      66 MFSCSMKSSHQKPSGCWQHISCNFPGCRTLAKYGQRQWKNKEDCWGTQELSCDLTSETSD 125
Db      48 -------IPNQSESTCYE---------VALLRYGIESWNSISNC--SQTLSYDLTAVTLD 89

Qy     126 I--QEPYYGRVRAASAGSYSEWSMT-PRFTPWWETKIDPPVMNITQV-----NGSLLVIL 177
Db      90 LYHSNGYRARVRAVDGSRHSNWTVTNTRFS------VDEVTLTVGSVNLEIHNGFILGKI 143

Qy     178 HAPNLPYRYQKEKNVSIEDYYELLYRVF-IINNSLEKEQKVYEGAHRAVEIEALTPHSS- 235
Db     144 QLP-------RPKMAPANDTYESIFSHFREYEIAIRKVPGNFTFTHKKVKHENFSLLTSG 196

Qy     236 ----YCVVAEIYQPMLDRRSQR---SEERCVEI 261
Db     197 EVGEFCVQV---KPSVASRSNKGMWSKEECISL 226


RESULT 6
A47003
cytokine receptor family class II protein CRF2-4 precursor - human
C;Species: Homo sapiens (man)
C;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 01-Dec-2000
C;Accession: A47003; G01418
R;Lutfalla, G.; Gardiner, K.; Uze, G.
Genomics 16, 366-373, 1993
A;Title: A new member of the cytokine receptor gene family maps on chromosome 21 at 1
A;Reference number: A47003; MUID:93300510; PMID:8314576
A;Accession: A47003
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-325 <LUT>
A;Cross-references: GB:Z17227; NID:g393378; PIDN:CAA78933.1; PID:g393379
R;Lutfalla, G.
submitted to the EMBL Data Library, April 1994
A;Reference number: G06935
A;Accession: G01418
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-123,'D',125-268,'VGRME' <LU2>
A;Cross-references: EMBL:U08988; NID:g571295; PID:g571296
C;Genetics:
A;Gene: GDB:CRFB4; CRF2-4
A;Cross-references: GDB:138168; OMIM:123889
A;Map position: 21q; 21q22.1-21q22.2
A;Introns: 17/1; 58/2; 111/1; 166/3; 216/1
C;Keywords: transmembrane protein

  Query Match            10.5%;  Score 149.5;  DB 2;  Length 325;
  Best Local Similarity  24.1%;  Pred. No. 1.4e-05;
  Matches   57;  Conservative   32;  Mismatches   89;  Indels   59;  Gaps    8;

Qy      30 PQRVQFQSRNFHNILQWQPGRALTGN--SSVYFVQYKIMFSCSMKSSHQKPSGCWQHISC 87
Db      24 PENVRMNSVNFKNILQWESPAFAKGNLTFTAQYLSYRIF---------------------- 62

Qy      88 NFPGCRTLAKYGQRQWKNKEDCWGTQELSCDLTSETSDIQEPYYG----RVRAASAGSYS 143
Db      63 ------------------QDKCMNTTLTECDFSSLSK------YGDHTLRVRAEFADEHS 98

Qy     144 EWSMTPRFTPWWETKIDPPVMNITQVNGSLLVILHAPNLPYRYQ--KEKNVSIEDYYELL 201
Db      99 DW-VNITFCPVDDTIIGPPGMQVEVLADSLHMRFLAPKIENEYETWTMKNV----YNSWT 153

Qy     202 YRVFIINNSLEKEQKVYEGAHRAVEIEALTPHSSYCVVAEIYQPMLDRRSQRSEERC 258
Db     154 YNVQYWKNGTDEKFQITPQYDFEV-LRNLEPWTTYCVQVRGFLPDRNKAGEWSEPVC 209


RESULT 7
KFBO3
tissue factor precursor - bovine
N;Alternate names: coagulation factor III
C;Species: Bos primigenius taurus (cattle)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 22-Jun-1999
C;Accession: JQ1319
R;Takayenoki, Y.; Muta, T.; Miyata, T.; Iwanaga, S.
Biochem. Biophys. Res. Commun. 181, 1145-1150, 1991
A;Title: cDNA and amino acid sequences of bovine tissue factor.
A;Reference number: JQ1319; MUID:92109720; PMID:1764065
A;Accession: JQ1319
```

```
A;Molecule type: mRNA
A;Residues: 1-292 <TAK>
A;Cross-references: GB:S74147; NID:g241438; PIDN:AAB20755.1; PID:g241439
A;Experimental source: adrenal gland
A;Note: part of this sequence, including the amino end of the mature protein, was confir
C;Comment: Tissue factor is an integral membrane glycoprotein that serves as a receptor
C;Comment: Expression of tissue factor can be induced in a variety of tissues by certain
C;Superfamily: tissue factor
C;Keywords: blood coagulation; glycoprotein; lipoprotein; thiolester bond; transmembrane
F;1-35/Domain: signal sequence #status predicted <SIG>
F;36-292/Product: tissue factor #status experimental <MAT>
F;36-248/Domain: extracellular #status predicted <EXT>
F;249-271/Domain: transmembrane #status predicted <TMM>
F;272-292/Domain: intracellular #status predicted <INT>
F;43,153,181/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;81-89,215-238/Disulfide bonds: #status predicted
F;118,124/Binding site: carbohydrate (Thr) (covalent) #status predicted
F;274/Binding site: palmitate (Cys) (covalent) #status experimental

 Query Match             9.7%;  Score 138.5;  DB 1;  Length 292;
 Best Local Similarity   22.6%;  Pred. No. 0.00011;
 Matches   59;  Conservative   43;  Mismatches  104;  Indels   55;  Gaps   12;

Qy      10 LISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVYFVQYKIMFSC 69
           |    |   ||   | : :    : ::| ||  ||:|:|       : || ||
Db      21 LFGLVLIQGAGVAGTTDVVVAYNITWKSTNFKTILEWEPKPI----NHVYTVQIS----- 71

Qy      70 SMKSSHQKPSGCWQHISCNFPGCRTLAKYGQRQWKNKEDCWGTQELSCDLTSE-TSDIQE 128
                                  : |   ||||  |: |    ||:| |   :::|
Db      72 -------------------------PRLG--NWKNK--CFYTTNTECDVTDEIVKNVRE 101

Qy     129 PYYGRVRAASAGSYSE----WSMTPRFTPWWETKI-DPPVMNITQVNGSLLVILHAPNL 182
            |  || :  | : |      :: :| |||: || :  | : :  ||   | | :
Db     102 TYLARVLSYPADTSSSTVEPPFTNSPEFTPYLETNLGQPTIQSFEQVGTKLNVTVQDART 161

Qy     183 PYRYQKEKNVSIEDYY--ELLYRVFIINNSLEKEQKVYEGAHR-AVEIEALTPHSSYC-- 237
             |      :|: | :  :| | ::    |   ::|     :   ::::      :||
Db     162 LVR-ANSAFLSLRDVFGKDLNYTLYYWKASSTGKKKATTNTNGFLIDVD---KGENYCFH 217

Qy     238 VVAEIYQPMLDRRSQRSEERC 258
           | | |    ::::|  |  :|
Db     218 VQAVILSRRVNQKSPESPIKC 238


RESULT 8
A32694
interferon alpha/beta receptor precursor - human
C;Species: Homo sapiens (man)
C;Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 22-Oct-1999
C;Accession: A32694; S17112
R;Uze, G.; Lutfalla, G.; Gresser, I.
Cell 60, 225-234, 1990
A;Title: Genetic transfer of a functional human interferon alpha receptor into mouse cel
A;Reference number: A32694; MUID:90124632; PMID:2153461
A;Accession: A32694
A;Molecule type: mRNA
A;Residues: 1-557 <UZE>
A;Cross-references: GB:J03171; NID:g184645; PIDN:AAA52730.1; PID:g306914
R;Lutfalla, G.
submitted to the EMBL Data Library, July 1991
A;Description: The structuree of the human interferon alpha/beta receptor gene.
A;Reference number: S17112
A;Accession: S17112
A;Molecule type: DNA
A;Residues: 1-16,'A',18-329,'V',343-557 <LUT>
A;Cross-references: EMBL:X60459; NID:g32671
C;Genetics:
A;Gene: GDB:IFNAR1; IFNAR; IFRC
A;Cross-references: GDB:120078; OMIM:107450
A;Map position: 21q22.1-21q22.1
A;Introns: 26/1; 67/2; 126/1; 177/3; 225/1; 263/2; 342/1; 381/3; 432/1; 480/3
C;Keywords: cytokine receptor; glycoprotein; transmembrane protein
F;1-21/Domain: transmembrane #status predicted <TRN1>
F;437-455/Domain: transmembrane #status predicted <TRN2>
F;50,58,81,88,110,172,254,313,314,376,416,433,507,518,537/Binding site: carbohydrate

 Query Match             9.6%;  Score 136.5;  DB 2;  Length 557;
 Best Local Similarity   20.8%;  Pred. No. 0.00039;
 Matches   54;  Conservative   39;  Mismatches  115;  Indels   51;  Gaps    7;

Qy       2 PKHCFLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVYFV 61
           | ||               |   :|   |: ::   :| : :|:|      |  :  : |
Db     217 PVHCI------------KTTVENELPPPENIEVSVQNQNYVLKWD----YTYANMTFQV 259

Qy      62 QYKIMFSCSMKSSHQKPSGCWQHISCNFPGCRTLAKYGQRQWKNKEDCWGTQELSCDLTS 121
           |:   |      :|                                  :||   ||   :   |
Db     260 QWLHAFLKRNPGNH----------------------LYKWKQIPDCENVKTTQCVFPQ 295

Qy     122 ETSDIQEPYYGRVRAASAGSYSEWSMTPRFTPWWETKIDPPVMNITQVNGSLLVILHAPN 181
                :  | ||:|:   : | ||   :|    :  : ||| ||  :: |  : : ||
Db     296 NVFQ-KGIYLLRVQASDGNNTSFWSEEIKFDTEIQAFLLPPVFNIRSLSDSFHIYIGAP- 353

Qy     182 LPYRYQKEKNVSIEDYYELLYRVFIINNSLEKEQKVYEGAHRAVEIEALTPHSSYCVVAE 241
                ::  |  :   | |:| :    |:   |:|: |     | :  | | : ||| |
Db     354 -----KQSGNTPVIQDYPLIYEIIFWENTSNAERKIIE-KKTDVTVPNLKPLTVYCVKAR 407

Qy     242 IY--QPMLDRRSQRSEERC 258
             :     |:: |  |:  |
Db     408 AHTMDEKLNKSSVFSDAVC 426


RESULT 9
A45283
interferon alpha/beta receptor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 25-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C;Accession: A45283; I48423; I48424; I48425; I48426; I48427; I48428; I48429
R;Uze, G.; Lutfalla, G.; Bandu, M.T.; Proudhon, D.; Mogensen, K.E.
Proc. Natl. Acad. Sci. U.S.A. 89, 4774-4778, 1992
A;Title: Behavior of a cloned murine interferon alpha/beta receptor expressed in homo
A;Reference number: A45283; MUID:92262522; PMID:1533935
A;Accession: A45283
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-590 <UZE>
A;Cross-references: GB:M89641; NID:g194111; PIDN:AAA37890.1; PID:g194112
A;Note: sequence extracted from NCBI backbone (NCBIN:102354, NCBIP:102357)
R;Lutfalla, G.; Uze, G.
Gene 148, 343-346, 1994
A;Title: Structure of the murine interferon alpha/beta receptor-encoding gene: high-f
A;Reference number: I48423; MUID:95047447; PMID:7958966
A;Accession: I48423
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 118-125 <RES>
A;Cross-references: EMBL:U06237; NID:g497103; PIDN:AAA65003.1; PID:g755810
A;Accession: I48424
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 127-224 <RE2>
A;Cross-references: EMBL:U06238; NID:g497104; PIDN:AAC01749.1; PID:g755811
A;Accession: I48425
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 243-264 <RE3>
A;Cross-references: EMBL:U06239; NID:g497106; PIDN:AAA65004.1; PID:g510261
A;Accession: I48426
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 265-375 <RE4>
A;Cross-references: EMBL:U06240; NID:g497108; PIDN:AAA65005.1; PID:g510262
A;Accession: I48427
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 397-424 <RE5>
A;Cross-references: EMBL:U06241; NID:g497110; PIDN:AAA65006.1; PID:g755812
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A;Accession: I48428
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 426-445 <RE6>
A;Cross-references: EMBL:U06242; NID:g497112; PIDN:AAA65007.1; PID:g755813
A;Accession: I48429
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 473-590 <RE7>
A;Cross-references: EMBL:U06244; NID:g497114; PIDN:AAA65008.1; PID:g510265
C;Genetics:
A;Gene: IFNAR
A;Introns: 177/3; 331/1
C;Keywords: cytokine receptor; transmembrane protein

  Query Match             9.4%;  Score 134.5;  DB 2;  Length 590;
  Best Local Similarity   21.4%;  Pred. No. 0.00063;
  Matches   45;  Conservative   39;  Mismatches   99;  Indels   27;  Gaps    7;

Qy      55 NSSVYFV--QYKIMFSCSMKSSHQKPSGCWQHISCNFPGCRTLAKY---GQRQWKNKEDC 109
           |  ||  :   | : :     |||  :  |     |  |      |:|    : :|    :|
Db      34 NIDVYIIDDNYTLKW-----SSHGESMG-----SVTFS-----AEYRTKDEAKWLKVPEC 78

Qy     110 WGTQELSCDLTSETSDIQEPYYGRVRAASAGSYSEWSMTPRFTPWWETKIDPPVMNITQV 169
           |    |: :   :::      ||||    | | |:    | |::   : || : :
Db      79 QHTTTTKCEFSLLDTNVYIKTQFRVRAEEGNSTSSWNEVDPFIPFYTAHMSPPEVRLEAE 138

Qy     170 NGSLLVILHAPNLPYRYQKEKNVSIEDYYELLYRVFIINNSLEKEQKVYEGAHRAVEIEA 229
           : ::|| :  |       :: |:   :     | : |   |   ::|     :   :|
Db     139 DKAILVHISPPG------QDGNMWALEKPSFSYTIRIWQKS-SSDKKTINSTYYVEKIPE 191

Qy     230 LTPHSSYCVVAEIYQPMLDRRSQRSEERCV 259
           | | ::||:  :   | | : |  |  :|:
Db     192 LLPETTYCLEVKAIHPSLKKHSNYSTVQCI 221


RESULT 10
KFRB3
tissue factor precursor - rabbit
N;Alternate names: coagulation factor III
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jul-2000
C;Accession: JU0441; S23681
R;Andrews, B.S.; Rehemtulla, A.; Fowler, B.J.; Edgington, T.S.; Mackman, N.
Gene 98, 265-269, 1991
A;Title: Conservation of tissue factor primary sequence among three mammalian species.
A;Reference number: JU0441; MUID:91200676; PMID:1840552
A;Accession: JU0441
A;Molecule type: mRNA
A;Residues: 1-292 <AND>
A;Cross-references: GB:M55390; NID:g165696; PIDN:AAA63469.1; PID:g165697
A;Experimental source: brain
R;Pawashe, A.; Ezekowitz, M.; Lin, T.C.; Horton, R.; Bach, R.; Konigsberg, W.
Thromb. Haemost. 66, 315-320, 1991
A;Title: Molecular cloning, characterization and expression of cDNA for rabbit brain tis
A;Reference number: S23681; MUID:92081032; PMID:1746002
A;Accession: S23681
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 33-292 <PAW>
A;Cross-references: EMBL:X53521; NID:g1495; PIDN:CAA37597.1; PID:g3980170
C;Comment: Tissue factor is an integral membrane glycoprotein that serves as a receptor
C;Comment: Expression of tissue factor can be induced in a variety of tissues by certain
C;Superfamily: tissue factor
C;Keywords: blood coagulation; glycoprotein; lipoprotein; thiolester bond; transmembrane
F;1-32/Domain: signal sequence #status predicted <SIG>
F;33-292/Product: tissue factor #status predicted <MAT>
F;33-249/Domain: extracellular #status predicted <EXT>
F;250-271/Domain: transmembrane #status predicted <TMM>
F;272-292/Domain: intracellular #status predicted <INT>
F;41,114,154,167,182/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;79-87,216-239/Disulfide bonds: #status predicted
F;274/Binding site: palmitate (Cys) (covalent) #status experimental

  Query Match             9.3%;  Score 132.5;  DB 1;  Length 292;
  Best Local Similarity   22.2%;  Pred. No. 0.00039;
  Matches   62;  Conservative   39;  Mismatches   89;  Indels   89;  Gaps   13;

Qy      10 LISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVYFVQYKIMFSC 69
           |: : |  ||     |  : :   : ::| ||  ||:|:|        |:  | | :  |
Db      21 LLGWLLAQVARAADT--TGRAYNLTWKSTNFKTILEWEP-------KSIDHV-YTVQIST 70

Qy      70 SMKSSHQKPSGCWQHISCNFPGCRTLAKYGQRQWKNKEDCWGTQELSCDLTSE-TSDIQE 128
            :::                                ||:|  |: | |  |||| |   |: :
Db      71 RLEN-----------------------------WKSK--CFLTAETECDLTDEVVKDVGQ 99

Qy     129 PYYGRV-----RAASAGSYSE---WSMTPRFTPWWETKIDPPV----------MNITQVN 170
           |  ||     |  :   : |   :  :| |||: :| :  |           :|:|  :
Db     100 TYMARVLSYPARNGNTTGFPEEPPFRNSPEFTPYLDTNLGQPTIQSFEQVGTKLNVTVQD 159

Qy     171 GSLLVILHAPNLPYR--YQKEKNVSIEDYYELLY-------RVFIINNSLEKEQKVYEGA 221
             ||  :   |  |  : |: |      | | |       :     |: |    | :|
Db     160 ARTLVRRNGTFLSLRAVFGKDLN------YTLYYWRASSTGKKTATTNTNEFLIDVDKGE 213

Qy     222 HRAVEIEALTPHSSYCVVAEIYQPMLDRRSQRSEERCVE 260
           :    ::|: |              :| ||| |   |
Db     214 NYCFSVQAVIPSR-------------KRKQRSPESLTE 238


RESULT 11
A31555
interferon gamma receptor precursor - human
C;Species: Homo sapiens (man)
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 23-Jul-1999
C;Accession: A31555
R;Aguet, M.; Dembic, Z.; Merlin, G.
Cell 55, 273-280, 1988
A;Title: Molecular cloning and expression of the human interferon-gamma receptor.
A;Reference number: A31555; MUID:89003065; PMID:2971451
A;Accession: A31555
A;Molecule type: mRNA
A;Residues: 1-489 <AGU>
A;Cross-references: GB:J03143; NID:g184650; PIDN:AAA52731.1; PID:g306915
C;Genetics:
A;Gene: GDB:IFNGR1; IFNGR
A;Cross-references: GDB:120688; OMIM:107470
A;Map position: 6q23-6q24
C;Superfamily: interferon gamma receptor
C;Keywords: cytokine receptor; transmembrane protein

  Query Match             8.6%;  Score 122.5;  DB 2;  Length 489;
  Best Local Similarity   20.1%;  Pred. No. 0.0057;
  Matches   56;  Conservative   49;  Mismatches  103;  Indels   71;  Gaps   10;

Qy       9 FLISFFLTGVA----GTQSTHESL--KPQRVQFQSRNFHNILQWQPGRALTGNSSVYFVQ 62
           ||:    : ||:    ||     |    |  |  :| | : |: |              :
Db       5 FLLPLVMQGVSRAEMGTADLGPSSVPTPTNVTIESYNMNPIVYW--------------E 49

Qy      63 YKIM-----FSCSMKSSHQKPSGCWQHISCNFPGCRTLAKYGQRQWKNKEDCWGTQELSC 117
           |:||     |:  :|:                          || :  :  : |       |
Db      50 YQIMPQVPVFTVEVKN----------------------YGVKNSEWIDACINISHHYC 85

Qy     118 DLTSETSDIQEPYYGRVRAASAGSYSEWSMTPRFTPWWETKIDPPVMNITQVNGSLLVIL 177
           :::    |     : ||:|      | :: :  |    : || || ::| :    ::: :
Db      86 NISDHVGDPSNSLWVRVKARVGQKESAYAKSEEFAVCRDGKIGPPKLDIRKEEKQIMIDI 145

Qy     178 HAPNLPYRYQKEKNVSIEDY------YELLYRVFIINNSLEKEQKVYE---------GAH 222
             |:: :    |: |   ||      |  :| |::  |  | : |:
Db     146 FHPSV-FVNGDEQEV---DYDPETTCYIRVYNVYVRMNGSEIQYKILTQKEDDCDEIQCQ 201

Qy     223 RAVEIEALTPHSSYCVVAEIYQPMLDRRSQRSEERCVEI 261
           |: : :|  :| ||| ||    :    :::|:| |: |
Db     202 LAIPVSSL--NSQYCVSAEGVLHVWGVTTEKSKEVCITI 238


RESULT 12
```

```
KFMS3
tissue factor precursor - mouse
N;Alternate names: coagulation factor III
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 22-Jun-1999
C;Accession: A32318; A39046
R;Hartzell, S.; Ryder, K.; Lanahan, A.; Lau, L.F.; Nathans, D.
Mol. Cell. Biol. 9, 2567-2573, 1989
A;Title: A growth factor-responsive gene of murine BALB/c 3T3 cells encodes a protein ho
A;Reference number: A32318; MUID:89343974; PMID:2761539
A;Accession: A32318
A;Molecule type: mRNA
A;Residues: 1-294 <HAR>
A;Cross-references: GB:M26071; NID:g201924; PIDN:AAA40414.1; PID:g201925
R;Ranganathan, G.; Blatti, S.P.; Subramaniam, M.; Fass, D.N.; Maihle, N.J.; Getz, M.J.
J. Biol. Chem. 266, 496-501, 1991
A;Title: Cloning of murine tissue factor and regulation of gene expression by transformi
A;Reference number: A39046; MUID:91093171; PMID:1985911
A;Accession: A39046
A;Molecule type: mRNA
A;Residues: 1-25,'I',27-294 <RAN>
A;Cross-references: GB:M57896; GB:J05713; NID:g201926; PIDN:AAA63400.1; PID:g201927
A;Note: 26-Thr was also found
C;Comment: Tissue factor is an integral membrane glycoprotein that serves as a receptor
C;Comment: Expression of tissue factor can be induced in a variety of tissues by certain
C;Superfamily: tissue factor
C;Keywords: blood coagulation; glycoprotein; lipoprotein; thiolester bond; transmembrane
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-294/Product: tissue factor #status predicted <MAT>
F;30-251/Domain: extracellular #status predicted <EXT>
F;252-274/Domain: transmembrane #status predicted <TMM>
F;37,57,169,200/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;75-83,218-241/Disulfide bonds: #status predicted
F;275/Binding site: palmitate (Cys) (covalent) #status experimental

  Query Match              8.5%;  Score 122;  DB 1;  Length 294;
  Best Local Similarity   22.7%;  Pred. No. 0.0033;
  Matches   64;  Conservative   36;  Mismatches  100;  Indels   82;  Gaps   13;

Qy       6 FLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVYFVQYKI 65
           ||| |:    :|  ||        |   : : | :|  ||:|||       :  | ||
Db      17 FLGCLL-LQVTAGAGIPE-----KAFNLTWISTDFKTILEWQP----KPTNYTYTVQ--- 63

Qy      66 MFSCSMKSSHQKPSGCWQHISCNFPGCRTLAKYGQRQWKNKEDCWGTQELSCDLTSE-TS 124
             | :|                          | ||||  |: | :  ||||  |
Db      64 ---ISDRS--------------------------RNWKNK--CFSTTDTECDLTDEIVK 91

Qy     125 DIQEPYYGRVRAASA--------------GSYSEWSMTPRFTPWWETKIDPPV------- 163
           |:   |  :| :                  |    ::  |:| |: :| :  ||
Db      92 DVTWAYEAKVLSVPRRNSVHGDGDQLVIHGEEPPFTNAPKFLPYRDTNLGQPVIQQFEQD 151

Qy     164 ---MNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYYELLYRVFIINNSLEKEQKVYEG 220
              :|:   :   ||  :   | |    |::     | : ||     :|  |:  :
Db     152 GRKLNVVVKDSLTLVRKNGTFLTLRQVFGKDLG----YIITYRK---GSSTGKKTNITNT 204

Qy     221 AHRAVEIEALTPHSSYC--VVAEIYQPMLDRRSQRSEERCVE 260
             ::::|      |||  | | |:    :: |  |   | |
Db     205 NEFSIDVE---EGVSYCFFVQAMIFSRKTNQNSPGSSTVCTE 243


RESULT 13
A49947
interferon gamma receptor beta subunit - mouse
N;Alternate names: IFN-gamma R beta chain; IFN-gamma R species-specific cofactor; type I
C;Species: Mus musculus (house mouse)
C;Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C;Accession: A49947
R;Hemmi, S.; Bohni, R.; Stark, G.; Di Marco, F.; Aguet, M.
Cell 76, 803-810, 1994
A;Title: A novel member of the interferon receptor family complements functionality of t
A;Reference number: A49947; MUID:94170381; PMID:8124717
A;Accession: A49947
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-332 <HEM>
A;Cross-references: GB:S69336; NID:g545841; PIDN:AAB30165.1; PID:g545842
A;Experimental source: early B-cell line Y16
A;Note: sequence extracted from NCBI backbone (NCBIN:145654, NCBIP:145656)
C;Keywords: cytokine receptor

  Query Match              7.7%;  Score 110.5;  DB 2;  Length 332;
  Best Local Similarity   20.2%;  Pred. No. 0.04;
  Matches   51;  Conservative   33;  Mismatches   99;  Indels   69;  Gaps   11;

Qy       9 FLISFFLTGVAGTQSTHESLK----PQRVQFQSRNFHNILQWQPGRALTG-NSSVYFVQY 63
           :| |  | |:    |: :|      |   :    |   || |:|  :       || |:|
Db       7 WLPSLLLCGLGAAASSPDSFSQLAAPLNPRLHLYNDEQILTWEPSPSSNDPRPVVYQVEY 66

Qy      64 KIMFSCSMKSSHQKPSGCWQHISCNFPGCRTLAKYGQRQWKNKEDCWGTQELSCDLT--S 121
             :              | |  :                    : :|    |  ||||
Db      67 SFI-----------DGSWHRLL------------------EPNCTDITETKCDLTGGG 95

Qy     122 ETSDIQEPY--YGRVRAASAGSYSEWSMTPRFTPWWETKIDPPV-MNITQVNGSLLV--- 175
                 |:  : ||||      |:|     |  :    : ||  :::|   |||::
Db      96 RLKLFPHPFTVFLRVRAKRGNLTSKWVGLEPFQHYENVTVGPPKNISVTPGKGSLVIHFS 155

Qy     176 ----ILHAPNLPYRYQKEKNVSIEDYYELLYRVFIINNSLEKEQKVYEGAHR--AVEIEA 229
              : |     |         :  |:|           | :|:  ||  :  :: :
Db     156 PPFDVFHGATFQY---------LVHYWE----------KSETQQEQVEGPFKSNSIVLGN 196

Qy     230 LTPHSSYCVVAE 241
           | |:  ||:  |
Db     197 LKPYRVYCLQTE 208


RESULT 14
I39073
interferon alpha-beta receptor, beta subunit long form - human
C;Species: Homo sapiens (man)
C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 01-Dec-2000
C;Accession: I39073; S59502
R;Domanski, P.; Witte, M.; Kellum, M.; Rubinstein, M.; Hackett, R.; Pitha, P.; Colamo
J. Biol. Chem. 270, 21606-21611, 1995
A;Title: Cloning and expression of a long form of the beta subunit of the interferon
A;Reference number: I39073; MUID:95394915; PMID:7665574
A;Accession: I39073
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-515 <RES>
A;Cross-references: EMBL:U29584; NID:g993040; PIDN:AAC50202.1; PID:g993041
R;Lutfalla, G.; Holland, S.J.; Cinato, E.; Monneron, D.; Reboul, J.; Rogers, N.C.; Sm
EMBO J. 14, 5100-5108, 1995
A;Title: Mutant U5A cells are complemented by an interferon-alpha-beta receptor subun
A;Reference number: S59501; MUID:96067138; PMID:7588638
A;Accession: S59502
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual
A;Molecule type: mRNA
A;Residues: 1-150,'M',152-515 <LUT>
A;Cross-references: GB:L41942; NID:g995292; PIDN:AAB46413.1; PID:g995293
C;Keywords: alternative splicing; cytokine receptor

  Query Match              7.3%;  Score 103.5;  DB 2;  Length 515;
  Best Local Similarity   20.3%;  Pred. No. 0.29;
  Matches   46;  Conservative   39;  Mismatches   99;  Indels   43;  Gaps    7;

Qy      38 RNFHNILQWQPGRALTGNSSVYFVQYKIMFSCSMKSSHQKPSGCWQHISCNFPGCRTLAK 97
           ||| :|| |:       | |:    | ::::   |
Db      46 RNFRSILSWE-----LKNHSIVPTHYTLLYTIMSK------------------------ 75

Qy      98 YGQRQWKNKEDCWGTQELSCDLTSETSDIQEPYYGRVRAASAGSYSEWSMTPRFTPWWET 157
                 |  ::|  |    ||||  |     | |   |    :|: : :| :  |    :
Db      76 --PEDLKVVKNCANTTRSFCDLTDEWRSTHEAYV-TVLEGFSGNTTLFSCSHNFWLAIDM 132

Qy     158 KIDPPVMNITQVNGSLLVILHAPNL-PYRYQKEKNVSIEDYYELLYRVFIINNSLEKEQK 216
             :||   |      : |::  |::     | : :: ||:  | : :        : | |
Db     133 SFEPPEFEIVGFTNHINVVVKFPSIVEEELQFDLSLVIEEQSEGIVK------KHKPEIK 186
```

```
Qy     217 VYEGAHRAVEIEALTPHSSYCVVAEIYQPMLDRRSQ-RSEERCVEIP 262
           :    |: | |:::|||   :|    | ::  :|  :|  :|
Db     187 GNMSGNFTYIIDKLIPNTNYCV--SVYLEHSDEQAVIKSPLKCTLLP 231


RESULT 15
A54295
interferon alpha/beta receptor precursor - human
C;Species: Homo sapiens (man)
C;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 05-Nov-1999
C;Accession: A54295
R;Novick, D.; Cohen, B.; Rubinstein, M.
Cell 77, 391-400, 1994
A;Title: The human interferon alpha/beta receptor: characterization and molecular clonin
A;Reference number: A54295; MUID:94236684; PMID:8181059
A;Accession: A54295
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-331 <NOV>
A;Cross-references: GB:X77722; NID:g488363; PIDN:CAA54785.1; PID:g488364
A;Keywords: cytokine receptor

  Query Match             7.1%;  Score 101.5;  DB 2;  Length 331;
  Best Local Similarity   20.3%;  Pred. No. 0.25;
  Matches   46;  Conservative   39;  Mismatches   99;  Indels   43;  Gaps    7;

Qy      38 RNFHNILQWQPGRALTGNSSVYFVQYKIMFSCSMKSSHQKPSGCWQHISCNFPGCRTLAK 97
           ||| :|| |:       | |:    | :::: |
Db      46 RNFRSILSWE-----LKNHSIVPTHYTLLYTIMSK------------------------ 75

Qy      98 YGQRQWKNKEDCWGTQELSCDLTSETSDIQEPYYGRVRAASAGSYSEWSMTPRFTPWWET 157
             |  ::|  |    ||||  |     | |   |    :|: : :| :  |    :
Db      76 --PEDLKVVKNCANTTRSFCDLTDEWRSTHEAYV-TVLEGFSGNTTLFSCSHNFWLAIDM 132

Qy     158 KIDPPVMNITQVNGSLLVILHAPNL-PYRYQKEKNVSIEDYYELLYRVFIINNSLEKEQK 216
           :||   |      : |::  |::     | : :: ||:  | : :          : | |
Db     133 SFEPPEFEIVGFTNHINVMVKFPSIVEEELQFDLSLVIEEQSEGIVK------KHKPEIK 186

Qy     217 VYEGAHRAVEIEALTPHSSYCVVAEIYQPMLDRRSQ-RSEERCVEIP 262
           :    |: | |:::|||   :|    | ::  :|  :|  :|
Db     187 GNMSGNFTYIIDKLIPNTNYCV--SVYLEHSDEQAVIKSPLKCTLLP 231


Search completed: December 22, 2002, 10:14:23
Job time : 46 secs
```

GenCore version 5.1.3

OM protein - protein search, using sw model

Run on: December 22, 2002, 09:12:37 ; Search time 25 Seconds
(without alignments)
434.672 Million cell updates/sec

Title: US-09-964-994-2
Perfect score: 1427
Sequence: 1 MPKHCFLGFLISFFLTGVAG.....YQPMLDRRSQRSEERCVEIP 262

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	164.5	11.5	575	1	I10R_MOUSE	Q61727 mus musculu
2	163	11.4	295	1	TF_HUMAN	P13726 homo sapien
3	158	11.1	560	1	INR1_BOVIN	Q04790 bos taurus
4	156	10.9	349	1	I10S_MOUSE	Q61190 mus musculu
5	152.5	10.7	578	1	I10R_HUMAN	Q13651 homo sapien
6	149.5	10.5	325	1	I10S_HUMAN	Q08334 homo sapien
7	138.5	9.7	292	1	TF_BOVIN	P30931 bos taurus
8	136.5	9.6	289	1	TF_CAVPO	Q9jlu8 cavia porce
9	136.5	9.6	557	1	INR1_HUMAN	P17181 homo sapien
10	136.5	9.6	560	1	INR1_SHEEP	Q28589 ovis aries
11	134.5	9.4	590	1	INR1_MOUSE	P33896 mus musculu
12	132.5	9.3	292	1	TF_RABIT	P24055 oryctolagus
13	128.5	9.0	295	1	TF_RAT	P42533 rattus norv
14	124	8.7	294	1	TF_MOUSE	P20352 mus musculu
15	122.5	8.6	489	1	INGR_HUMAN	P15260 homo sapien
16	115	8.1	536	1	INR2_SHEEP	Q95207 ovis aries
17	104	7.3	530	1	INR2_BOVIN	Q95141 bos taurus
18	101.5	7.1	515	1	INR2_HUMAN	P48551 homo sapien
19	92	6.4	337	1	INGS_HUMAN	P38484 homo sapien
20	92	6.4	1254	1	POLS_RRVT	P08491 ross river
21	90.5	6.3	424	1	KPSH_HUMAN	P11801 homo sapien
22	90	6.3	1253	1	POLS_SFV	P03315 semliki for
23	88.5	6.2	1170	1	TSP2_BOVIN	Q95116 bos taurus
24	87.5	6.1	676	1	KALM_CHICK	P33005 gallus gall
25	86	6.0	477	1	INGR_MOUSE	P15261 mus musculu
26	85	6.0	792	1	RIR1_HUMAN	P23921 homo sapien
27	84.5	5.9	274	1	VC06_SPVKA	P32226 swinepox vi
28	82.5	5.8	478	1	HLY4_ECOLI	P09986 escherichia
29	81	5.7	564	1	YUES_CAEEL	P90859 caenorhabdi
30	81	5.7	810	1	CAN3_CHICK	Q92177 gallus gall
31	81	5.7	1247	1	POLS_ONNVG	P22056 o'nyong-nyo
32	80.5	5.6	478	1	HLYD_ECOLI	P06739 escherichia
33	80	5.6	582	1	KICH_YEAST	P20485 saccharomyc
34	79.5	5.6	1411	1	Y297_HUMAN	O15040 homo sapien
35	79	5.5	410	1	CPXI_BACME	P14762 bacillus me
36	79	5.5	606	1	Z214_HUMAN	Q9u159 homo sapien
37	78.5	5.5	576	1	GRK6_RAT	P97711 rattus norv
38	78.5	5.5	760	1	YBIL_ECOLI	P75780 escherichia
39	78.5	5.5	1003	1	POL_HV1N5	P12497 human immun
40	78	5.5	626	1	HCYD_EURCA	P02241 eurypelma c
41	78	5.5	1254	1	POLS_RRVN	P13890 ross river
42	77.5	5.4	526	1	CATA_HUMAN	P04040 homo sapien
43	77.5	5.4	638	1	GHR_HUMAN	P10912 homo sapien
44	77.5	5.4	897	1	CYRB_HUMAN	P32927 homo sapien
45	77.5	5.4	1172	1	TSP2_HUMAN	P35442 homo sapien

ALIGNMENTS

RESULT 1
I10R_MOUSE
ID I10R_MOUSE STANDARD; PRT; 575 AA.
AC Q61727;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Interleukin-10 receptor alpha chain precursor (IL-10R-A) (IL-10R1).
GN IL10RA OR IL10R.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6 X AJ F1; TISSUE=Hematopoietic;
RX MEDLINE=94068585; PubMed=8248239;
RA Ho A.S.-Y., Liu Y., Khan T.A., Hsu D.-H., Bazan J.F., Moore K.W.;
RT "A receptor for interleukin 10 is related to interferon receptors.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:11267-11271(1993).
CC -!- FUNCTION: RECEPTOR FOR IL-10; BINDS IL-10 WITH A HIGH AFFINITY.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
CC ---

CC ---
DR EMBL; L12120; AAA16156.1; -.
DR MGD; MGI:96538; Il10ra.
DR InterPro; IPR000282; Cytok_receptor_2.
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 16 POTENTIAL.
FT CHAIN 17 575 INTERLEUKIN-10 RECEPTOR ALPHA CHAIN.
FT DOMAIN 17 241 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 242 262 POTENTIAL.
FT DOMAIN 263 575 CYTOPLASMIC (POTENTIAL).
FT DISULFID 204 225 POTENTIAL.
FT CARBOHYD 50 50 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 66 66 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 113 113 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 182 182 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 575 AA; 64248 MW; 820B9CD576F686B7 CRC64;

Query Match 11.5%; Score 164.5; DB 1; Length 575;
Best Local Similarity 26.7%; Pred. No. 1.8e-07;
Matches 74; Conservative 37; Mismatches 89; Indels 77; Gaps 16;

```
Qy      6 FLGFLISFFLTGVA-GTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVYFVQYK 64
          ||  : |  |  :| ||     |   |  | |::| | :|| |:|      : | |   |:
Db      8 FLVTISSLSLEFIAYGT----ELPSPSYVWFEARFFQHILHWKP--IPNQSESTY---YE 58
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```
Qy      65 IMFSCSMKSSHQKPSGCWQHISCNFPGCRTLAKYGQRQWKNKEDCWGTQELSCDLTSETS 124
           :                              | :||   | :   |   | ||||||: |
Db      59 V----------------------------ALKQYGNSTWNDIHICRKAQALSCDLTTFTL 90

Qy     125 DIQEPYYG---RVRAASAGSYSEWSMT-PRFTPWWETKIDPPVMNITQV-----NGSLLV 175
           |:    ||   ||||     || |: |  |||      :|  :: :  |     :| :
Db      91 DLYHRSYGYRARVRAVDNSQYSNWTTTETRFT------VDEVILTVDSVTLKAMDGIIYG 144

Qy     176 ILHAPNLPYRYQKEKNVSIEDYYELLY---RVFIINNSLEKEQKVYEGAHRAVEIEALT- 231
           :| |       :       | || ::   ||: |  |: |  :: : | : |: |  |
Db     145 TIHPP-------RPTITPAGDEYEQVFKDLRVYKI--SIRKFSEL-KNATKRVKQETFTL 194

Qy     232 ----PHSSYCVVAEIYQPMLDRR---SQRSEERCVEI 261
                  :||      | |: |   :: |||:|: |
Db     195 TVPIGVRKFCVKV---LPRLESRINKAEWSEEQCLLI 228
```

RESULT 2
[redacted]HUMAN
TF_HUMAN STANDARD; PRT; 295 AA.
P13726;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Tissue factor precursor (TF) (Coagulation factor III)
DE (Thromboplastin) (CD142 antigen).
GN F3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89247359; PubMed=2719931;
RA Mackman N., Morrissey J.H., Fowler B., Edgington T.S.;
RT "Complete sequence of the human tissue factor gene, a highly
RT regulated cellular receptor that initiates the coagulation protease
RT cascade.";
RL Biochemistry 28:1755-1762(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87260946; PubMed=3037536;
RA Spicer E.K., Horton R., Bloem L., Bach R., Williams K.R., Guha A.,
RA Kraus J., Lin T.C., Nemerson Y., Konigsberg W.H.;
RT "Isolation of cDNA clones coding for human tissue factor: primary
RT structure of the protein and cDNA.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:5148-5152(1987).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=87244317; PubMed=3297348;
RA Morrissey J.H., Fakhrai H., Edgington T.S.;
RT "Molecular cloning of the cDNA for tissue factor, the cellular
RT receptor for the initiation of the coagulation protease cascade.";
RL Cell 50:129-135(1987).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=88050796; PubMed=2823875;
RA Scarpati E.M., Wen D., Broze G.J. Jr., Miletich J.P.,
RA Flandermeyer R.R., Siegel N.R., Sadler J.E.;
RT "Human tissue factor: cDNA sequence and chromosome localization of
RT the gene.";
RL Biochemistry 26:5234-5238(1987).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=88100453; PubMed=3424286;
RA Fisher K.L., Gorman C.M., Vehar G.A., O'Brien D.P., Lawn R.M.;
RT "Cloning and expression of human tissue factor cDNA.";
RL Thromb. Res. 48:89-99(1987).
RN [6]
RP DISULFIDE BONDS, AND PALMITOYLATION.
RX MEDLINE=89000604; PubMed=3166978;
RA Bach R., Konigsberg W.H., Nemerson Y.;
RT "Human tissue factor contains thioester-linked palmitate and stearate
RT on the cytoplasmic half-cystine.";
RL Biochemistry 27:4227-4231(1988).
RN [7]
RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS) OF 33-243.
RX MEDLINE=94368785; PubMed=8086403;
RA Muller Y.A., Ultsch M.H., Kelley R.F., de Vos A.M.;
RT "Structure of the extracellular domain of human tissue factor:
RT location of the factor VIIa binding site.";
RL Biochemistry 33:10864-10870(1994).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF 33-243.
RX MEDLINE=96190957; PubMed=8609606;
RA Muller Y.A., Ultsch M.H., de Vos A.M.;
RT "The crystal structure of the extracellular domain of human tissue
RT factor refined to 1.7-A resolution.";
RL J. Mol. Biol. 256:144-159(1996).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 33-251 IN COMPLEX WITH FVIIA.
RX MEDLINE=96175641; PubMed=8598903;
RA Banner D.W., D'Arcy A., Chene C., Winkler F.K., Guha A.,
RA Konigsberg W.H., Nemreson Y., Kirchhofer D.;
RT "The crystal structure of the complex of blood coagulation factor
RT VIIa with soluble tissue factor.";
RL Nature 380:41-46(1996).
RN [10]
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 37-242 IN COMPLEX WITH FVIIA.
RX MEDLINE=99126538; PubMed=9925787;
RA Zhang E., St Charles R., Tulinsky A.;
RT "Structure of extracellular tissue factor complexed with factor VIIa
RT inhibited with a BPTI mutant.";
RL J. Mol. Biol. 285:2089-2104(1999).
CC -!- FUNCTION: INITIATES BLOOD COAGULATION BY FORMING A COMPLEX WITH
CC CIRCULATING FACTOR VII OR VIIA. THE [TF:VIIA] COMPLEX ACTIVATES
CC FACTORS IX OR X BY SPECIFIC LIMITED PROTOLYSIS. TF PLAYS A ROLE IN
CC NORMAL HEMOSTASIS BY INITIATING THE CELL-SURFACE ASSEMBLY AND
CC PROPAGATION OF THE COAGULATION PROTEASE CASCADE.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- INDUCTION: TF EXPRESSION IS HIGHLY DEPENDENT UPON CELL TYPE. TF
CC CAN ALSO BE INDUCED BY THE INFLAMMATORY MEDIATORS INTERLEUKIN 1
CC AND TNF, AS WELL AS BY ENDOTOXIN, TO APPEAR ON MONOCYTES AND
CC VASCULAR ENDOTHELIAL CELLS AS A COMPONENT OF CELLULAR IMMUNE
CC RESPONSE.
CC -!- SIMILARITY: BELONGS TO THE TISSUE FACTOR FAMILY.
CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD142 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd142.htm".
CC ---

CC ---
DR EMBL; J02931; AAA61150.1; -.
DR EMBL; M16553; AAA61151.1; -.
DR EMBL; J02846; AAA61152.1; -.
DR EMBL; M27436; AAA36734.1; -.
DR EMBL; A19048; CAA01438.1; -.
DR PIR; A28320; KFHU3.
DR PIR; A43645; A43645.
DR PIR; A47574; A47574.
DR PDB; 1BOY; 10-JUN-96.
DR PDB; 2HFT; 29-JAN-96.
DR PDB; 1DAN; 04-SEP-97.
DR PDB; 1AHW; 19-AUG-98.
DR PDB; 1TFH; 19-AUG-98.
DR PDB; 1FAK; 03-DEC-99.
DR Genew; HGNC:3541; F3.
DR MIM; 134390; -.
DR InterPro; IPR000282; Cytok_receptor_2.
DR InterPro; IPR001187; Tissue_factor.

```
DR   Pfam; PF01108; Tissue_fac; 1.
DR   PRINTS; PR00346; TISSUEFACTOR.
DR   PROSITE; PS00621; TISSUE_FACTOR; 1.
KW   Glycoprotein; Blood coagulation; Transmembrane; Signal; Lipoprotein;
KW   Palmitate; 3D-structure; Polymorphism.
FT   SIGNAL        1     32
FT   CHAIN        33    295       TISSUE FACTOR.
FT   DOMAIN       33    251       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    252    274       POTENTIAL.
FT   DOMAIN      275    295       CYTOPLASMIC (POTENTIAL).
FT   SITE         46     48       WKS MOTIF.
FT   SITE         77     79       WKS MOTIF.
FT   SITE        190    192       WKS MOTIF.
FT   CARBOHYD    156    156       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    169    169       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   DISULFID     81     89
FT   DISULFID    218    241
FT   LIPID       277    277       PALMITATE.
FT   VARIANT     163    163       R -> W (IN DBSNP:5901).
                                  /FTId=VAR_012008.
FT   CONFLICT    260    260       V -> A (IN REF. 4).
     SEQUENCE   295 AA;  33067 MW;  D3486C713ED8EAD0 CRC64;

  Query Match            11.4%;  Score 163;  DB 1;  Length 295;
  Best Local Similarity  23.4%;  Pred. No. 1.1e-07;
  Matches   62;  Conservative   45;  Mismatches  100;  Indels   58;  Gaps   13;

Qy      10 LISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVYFVQYKIMFSC 69
           |: :    |||   |  ::    : ::| ||  ||:|:|       : || ||
Db      21 LLGWVFAQVAGASGTTNTVAAYNLTWKSTNFKTILEWEPKPV----NQVYTVQ------I 70

Qy      70 SMKSSHQKPSGCWQHISCNFPGCRTLAKYGQRQWKNKEDCWGTQELSCDLTSE-TSDIQE 128
           | ||                          ||:|  |: | :  |||| |   |:::
Db      71 STKSG-------------------------DWKSK--CFYTTDTECDLTDEIVKDVKQ 101

Qy     129 PYYGRV------RAASAGSYSE--WSMTPRFTPWWETKI-DPPVMNITQVNGSLLVILHA 179
           |  ||         | ||  |  :  :| |||: || :  | : :  ||   : | :
Db     102 TYLARVFSYPAGNVESTGSAGEPLYENSPEFTPYLETNLGQPTIQSFEQVGTKVNVTVED 161

Qy     180 PNLPYRYQKEKNVSIEDYY--ELLYRVFIINNSLEKEQKVYEGAHR-AVEIEALTPHSSY 236
           | :    :|: | :  :|:| ::   :|   ::      :   ::::      :|
Db     162 ERTLVR-RNNTFLSLRDVFGKDLIYTLYYWKSSSSGKKTAKTNTNEFLIDVD---KGENY 217

Qy     237 C--VVAEIYQPMLDRRSQRSEERCV 259
           |  | | |    ::|:|  |   |:
Db     218 CFSVQAVIPSRTVNRKSTDSPVECM 242


ULT 3
1_BOVIN
ID   INR1_BOVIN     STANDARD;      PRT;   560 AA.
AC   Q04790;
DT   01-OCT-1993 (Rel. 27, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   01-NOV-1997 (Rel. 35, Last annotation update)
DE   Interferon-alpha/beta receptor alpha chain precursor (IFN-alpha-REC).
GN   IFNAR1 OR IFNAR.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RX   MEDLINE=93076908; PubMed=1446745;
RA   Mouchel-Vielh E., Lutfalla G., Mogensen K.E., Uze G.;
RT   "Specific antiviral activities of the human alpha interferons are
RT   determined at the level of receptor (IFNAR) structure.";
RL   FEBS Lett. 313:255-259(1992).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93305725; PubMed=8318540;
RA   Lim J.-K., Langer J.A.;
RT   "Cloning and characterization of a bovine alpha interferon receptor.";
RL   Biochim. Biophys. Acta 1173:314-319(1993).
CC   -!- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPE
CC       I IFNS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS
CC       INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA-AND BETA-
CC       SUBUNITS THEMSELVES.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC   -!- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
CC   ---------------------------------------------------------------------
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CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X68443; CAA48484.1; -.
DR   EMBL; L06320; AAA02571.1; -.
DR   PIR; S33770; S33770.
DR   PIR; S27387; S27387.
DR   InterPro; IPR000282; Cytok_receptor_2.
DR   InterPro; IPR001187; Tissue_factor.
DR   Pfam; PF01108; Tissue_fac; 1.
KW   Receptor; Transmembrane; Glycoprotein; Signal.
FT   SIGNAL        1     24       BY SIMILARITY.
FT   CHAIN        25    560       INTERFERON-ALPHA/BETA RECEPTOR ALPHA
FT                                CHAIN.
FT   DOMAIN       25    437       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    438    458       POTENTIAL.
FT   DOMAIN      459    560       CYTOPLASMIC (POTENTIAL).
FT   DISULFID     76     84       BY SIMILARITY.
FT   DISULFID    199    220       BY SIMILARITY.
FT   CARBOHYD     47     47       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     55     55       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     85     85       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    109    109       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    172    172       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    254    254       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    313    313       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    377    377       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    434    434       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT    422    422       F -> V (IN REF. 2).
SQ   SEQUENCE   560 AA;  63818 MW;  66D76B72861E1D11 CRC64;

  Query Match            11.1%;  Score 158;  DB 1;  Length 560;
  Best Local Similarity  24.1%;  Pred. No. 6.7e-07;
  Matches   57;  Conservative   38;  Mismatches  100;  Indels   42;  Gaps    8;

Qy      21 TQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVYFVQYKIMFSCSMKSSHQKPSG 80
           |   |:   |: :|  : |   :|:|         :: :  |:   |   :  :|
Db     223 TTERHKVPSPENIQINADNQIYVLKWD----YPYENATFQAQWLRAFFKKIPGNHSD--- 275

Qy      81 CWQHISCNFPGCRTLAKYGQRQWKNKEDCWGTQELSCDLTSETSDIQEPYYGRVRAASAG 140
                              :||   :|      |    | |  :  || ||||::
Db     276 --------------------KWKQIPNCENVTSTHCVFPREVSS-RGIYYVRVRASNGN 313

Qy     141 SYSEWSMTPRFTPWWETKIDPPVMNITQV-NGSLLVILHAPNLPYRYQKEKNVSIEDYYE 199
             | ||    |    :| | |||:::  | : || | : |       :: :|:|:   |
Db     314 GTSFWSEEKEFNTEMKTIIFPPVISVKSVTDDSLHVSVGAS------EESENMSVNQLYP 367

Qy     200 LLYRVFIINNSLEKEQKVYEGAHRAVEIEALTPHSSYCVVAEIYQPML--DRRSQRS 254
           |:| |    |:   |:|| |     :    | | : ||| |   : ::  |||:: |
Db     368 LIYEVIFWENTSNAERKVLEKRTNFI-FPDLKPLTVYCVKA---RALIENDRRNKGS 420


RESULT 4
I10S_MOUSE
ID   I10S_MOUSE     STANDARD;      PRT;   349 AA.
AC   Q61190;
DT   16-OCT-2001 (Rel. 40, Created)
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DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Interleukin-10 receptor beta chain precursor (IL-10R-B) (IL-10R2)
DE   (Cytokine receptor class-II CRF2-4).
GN   IL10RB OR CRFB4.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97199375; PubMed=9047351;
RA   Gibbs V.C., Pennica D.;
RT   "CRF2-4: isolation of cDNA clones encoding the human and mouse
RT   proteins.";
RL   Gene 186:97-101(1997).
RN   [2]
RP   CHARACTERIZATION.
RX   MEDLINE=98130620; PubMed=9463407;
RA   Spencer S.D., Di Marco F., Hooley J., Pitts-Meek S., Bauer M.,
RA   Ryan A.M., Sordat B., Gibbs V.C., Aguet M.;
RT   "The orphan receptor CRF2-4 is an essential subunit of the interleukin
RT   10 receptor.";
RL   J. Exp. Med. 187:571-578(1998).
CC   -!- FUNCTION: RECEPTOR FOR IL-10 AND IL-22. SERVES AS AN ACCESSORY
CC       CHAIN ESSENTIAL FOR THE ACTIVE IL-10 RECEPTOR COMPLEX AND TO
CC       INITIATE IL-10-INDUCED SIGNAL TRANSDUCTION EVENTS.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC   -!- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U53696; AAC53062.1; -.
DR   MGD; MGI:109380; Il10rb.
DR   InterPro; IPR000282; Cytok_receptor_2.
DR   InterPro; IPR003961; FN_III.
DR   SMART; SM00060; FN3; 1.
KW   Receptor; Transmembrane; Glycoprotein; Signal.
FT   SIGNAL       1    19       POTENTIAL.
FT   CHAIN       20   349       INTERLEUKIN-10 RECEPTOR BETA CHAIN.
FT   DOMAIN      20   220       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   221   241       POTENTIAL.
FT   DOMAIN     242   349       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN     113   205       FIBRONECTIN TYPE-III.
FT   DISULFID    66    74       BY SIMILARITY.
FT   DISULFID   188   209       BY SIMILARITY.
FT   CARBOHYD    49    49       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   102   102       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   161   161       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   199   199       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   349 AA;  39774 MW;  58BA4F6B86330A39 CRC64;

  Query Match             10.9%;  Score 156;  DB 1;  Length 349;
  Best Local Similarity   26.8%;  Pred. No. 5.8e-07;
  Matches   72;  Conservative   30;  Mismatches   89;  Indels   78;  Gaps   13;

Qy       5 CFLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQ----PGRALTGNSSVYF 60
           |  |:|  | |    |        |::|:  | || |||||:    |   ||     :
Db       4 CVAGWLGGFLLVPALGMIP-----PPEKVRMNSVNFKNILQWEVPAFPKTNLT-----FT 53

Qy      61 VQYKIMFS----CSMKSSHQKPSGCWQHISCNFPGCRTLAKYGQRQWKNKEDCWGTQELS 116
             ||:   |    |   :| |          |:|     |:|||
Db      54 AQYESYRSFQDHCKRTASTQ----------CDF---SHLSKYGD---------------- 84

Qy     117 CDLTSETSDIQEPYYGRVRAASAGSYSEWSMTPRFTPWWETKIDPPVMNITQVNGSLLVI 176
                   |  ||||  |  :||| :   | |  :| | || | |  :  || :

Db      85 ------------YTVRVRAELADEHSEW-VNVTFCPVEDTIIGPPEMQIESLAESLHLR 130

Qy     177 LHAPNLPYRYQKE------KNVSIEDYYELLYRV-FIINNSLEKEQKVYEGAHRAVEIEA 229
             || :    : |       ||:    |    ||| :  | : || | |    : :  :
Db     131 FSAPQI----ENEPETWTLKNI----YDSWAYRVQYWKNGTNEKFQVV--SPYDSEVLRN 180

Qy     230 LTPHSSYCVVAEIYQPMLDRRSQRSEERC 258
           | | ::||:  : :    :|  : ||  |
Db     181 LEPWTTYCIQVQGFLLDQNRTGEWSEPIC 209


RESULT 5
I10R_HUMAN
ID   I10R_HUMAN     STANDARD;      PRT;   578 AA.
AC   Q13651;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Interleukin-10 receptor alpha chain precursor (IL-10R-A) (IL-10R1).
GN   IL10RA OR IL10R.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lymphoma;
RX   MEDLINE=94165477; PubMed=8120391;
RA   Liu Y., Wei S.H.-Y., Ho A.S.-Y., de Waal Malefyt R., Moore K.W.;
RT   "Expression cloning and characterization of a human IL-10 receptor.";
RL   J. Immunol. 152:1821-1829(1994).
CC   -!- FUNCTION: RECEPTOR FOR IL-10; BINDS IL-10 WITH A HIGH AFFINITY.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- TISSUE SPECIFICITY: SPLEEN, THYMUS, AND PBMC. FAINT EXPRESSION
CC       IN PANCREAS, SKELETAL MUSCLE, BRAIN, HEART, AND KIDNEY. PLACENTA,
CC       LUNG, AND LIVER SHOWED INTERMEDIATE LEVELS. MONOCYTES, B CELLS,
CC       LARGE GRANULAR LYMPHOCYTES, AND T CELLS EXPRESS HIGH LEVELS OF IL-
CC       10R.
CC   -!- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U00672; AAA17896.1; -.
DR   Genew; HGNC:5964; IL10RA.
DR   MIM; 146933; -.
DR   InterPro; IPR000282; Cytok_receptor_2.
KW   Receptor; Transmembrane; Glycoprotein; Signal.
FT   SIGNAL       1    21       POTENTIAL.
FT   CHAIN       22   578       INTERLEUKIN-10 RECEPTOR ALPHA CHAIN.
FT   DOMAIN      22   235       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   236   256       POTENTIAL.
FT   DOMAIN     257   578       CYTOPLASMIC (POTENTIAL).
FT   DISULFID   202   223       POTENTIAL.
FT   CARBOHYD    50    50       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    74    74       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   110   110       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   154   154       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   177   177       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   189   189       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   578 AA;  62903 MW;  EE1B29064338157C CRC64;

  Query Match             10.7%;  Score 152.5;  DB 1;  Length 578;
  Best Local Similarity   24.5%;  Pred. No. 2.2e-06;
  Matches   67;  Conservative   39;  Mismatches   94;  Indels   73;  Gaps   14;

Qy       7 LGFLISFFLTGVA-GTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVYFVQYKI 65
           |  |:|  |   | ||    |   |  | |::  ||:|| | |
```

```
Db       9 LAALLSLRLGSDAHGT----ELPSPPSVWFEAEFFHHILHWTP---------------- 47

Qy      66 MFSCSMKSSHQKPSGCWQHISCNFPGCRTLAKYGQRQWKNKEDCWGTQELSCDLTSETSD 125
                :|  | |::           | :||   | :  :|  :| || |||: | |
Db      48 -------IPNQSESTCYE---------VALLRYGIESWNSISNC--SQTLSYDLTAVTLD 89

Qy     126 I--QEPYYGRVRAASAGSYSEWSMT-PRFTPWWETKIDPPVMNITQV-----NGSLLVIL 177
           :     |  ||||     :| |::|  ||:      :|   : :  |     || :|  :
Db      90 LYHSNGYRARVRAVDGSRHSNWTVTNTRFS------VDEVTLTVGSVNLEIHNGFILGKI 143

Qy     178 HAPNLPYRYQKEKNVSIEDYYELLYRVF-IINNSLEKEQKVYEGAHRAVEIEALTPHSS- 235
             |      : |     | || ::  |     :: |    :   |: |: | :  :|
Db     144 QLP-------RPKMAPANDTYESIFSHFREYEIAIRKVPGNFTFTHKKVKHENFSLLTSG 196

Qy     236 ----YCVVAEIYQPMLDRRSQR---SEERCVEI 261
                :||     :| :  || :   |:| |: :
Db     197 EVGEFCVQV---KPSVASRSNKGMWSKEECISL 226
```

RESULT 6
[redacted]_HUMAN
ID I10S_HUMAN STANDARD; PRT; 325 AA.
AC Q08334;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Interleukin-10 receptor beta chain precursor (IL-10R-B) (IL-10R2)
DE (Cytokine receptor class-II CRF2-4).
GN IL10RB OR CRFB4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal brain;
RX MEDLINE=93300510; PubMed=8314576;
RA Lutfalla G., Gardiner K., Uze G.;
RT "A new member of the cytokine receptor gene family maps on chromosome
RT 21 at less than 35 kb from IFNAR.";
RL Genomics 16:366-373(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96054036; PubMed=7563119;
RA Lutfalla G., McInnis M.G., Antonarakis S.E., Uze G.;
RT "Structure of the human CRFB4 gene: comparison with its IFNAR
RT neighbor.";
RL J. Mol. Evol. 41:338-344(1995).
RN [3]
CHARACTERIZATION.
RX MEDLINE=97459974; PubMed=9312047;
RA Kotenko S.V., Krause C.D., Izotova L.S., Pollack B.P., Wu W.,
RA Pestka S.;
RT "Identification and functional characterization of a second chain of
RT the interleukin-10 receptor complex.";
RL EMBO J. 16:5894-5903(1997).
RN [4]
RP CHARACTERIZATION.
RX MEDLINE=20469498; PubMed=10875937;
RA Xie M.-H., Aggarwal S., Ho W.-H., Foster J., Zhang Z., Stinson J.,
RA Wood W.I., Goddard A.D., Gurney A.L.;
RT "Interleukin (IL)-22, a novel human cytokine that signals through the
RT interferon receptor-related proteins CRF2-4 and IL-22R.";
RL J. Biol. Chem. 275:31335-31339(2000).
CC -!- FUNCTION: RECEPTOR FOR IL-10 AND IL-22. SERVES AS AN ACCESSORY
CC CHAIN ESSENTIAL FOR THE ACTIVE IL-10 RECEPTOR COMPLEX AND TO
CC INITIATE IL-10-INDUCED SIGNAL TRANSDUCTION EVENTS.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -!- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
CC --
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CC --
DR EMBL; Z17227; CAA78933.1; -.
DR EMBL; U08988; AAA86872.1; -.
DR PIR; A47003; A47003.
DR HSSP; P13726; 1TFH.
DR Genew; HGNC:5965; IL10RB.
DR MIM; 123889; -.
DR InterPro; IPR000282; Cytok_receptor_2.
DR InterPro; IPR001187; Tissue_factor.
DR Pfam; PF01108; Tissue_fac; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 325 INTERLEUKIN-10 RECEPTOR BETA CHAIN.
FT DOMAIN 20 220 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 221 242 POTENTIAL.
FT DOMAIN 243 325 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 113 205 FIBRONECTIN TYPE-III.
FT DISULFID 66 74 BY SIMILARITY.
FT DISULFID 188 209 BY SIMILARITY.
FT CARBOHYD 49 49 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 68 68 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 102 102 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 161 161 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 124 124 A -> D (IN REF. 2).
FT CONFLICT 269 273 FLGHP -> VGRME (IN REF. 2).
FT CONFLICT 274 325 MISSING (IN REF. 2).
SQ SEQUENCE 325 AA; 37011 MW; 66706C79F8514B23 CRC64;

Query Match 10.5%; Score 149.5; DB 1; Length 325;
Best Local Similarity 24.1%; Pred. No. 2.1e-06;
Matches 57; Conservative 32; Mismatches 89; Indels 59; Gaps 8;

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Qy      30 PQRVQFQSRNFHNILQWQPGRALTGN--SSVYFVQYKIMFSCSMKSSHQKPSGCWQHISC 87
           |: |:  | || |||||:      ||   :  :: |:|
Db      24 PENVRMNSVNFKNILQWESPAFAKGNLTFTAQYLSYRIF-------------------- 62

Qy      88 NFPGCRTLAKYGQRQWKNKEDCWGTQELSCDLTSETSDIQEPYYG----RVRAASAGSYS 143
                              :: |  |    || :| :       ||    ||||  |  :|
Db      63 ------------------QDKCMNTTLTECDFSSLSK------YGDHTLRVRAEFADEHS 98

Qy     144 EWSMTPRFTPWWETKIDPPVMNITQVNGSLLVILHAPNLPYRYQ--KEKNVSIEDYYELL 201
           :| :   | |  :| | || | :  :  || :   || :   |:    |||    |
Db      99 DW-VNITFCPVDDTIIGPPGMQVEVLADSLHMRFLAPKIENEYETWTMKNV----YNSWT 153

Qy     202 YRVFIINNSLEKEQKVYEGAHRAVEIEALTPHSSYCVVAEIYQPMLDRRSQRSEERC 258
           | |    |  ::: ::       | :  | | ::|||    : |  ::  : ||  |
Db     154 YNVQYWKNGTDEKFQITPQYDFEV-LRNLEPWTTYCVQVRGFLPDRNKAGEWSEPVC 209
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RESULT 7
TF_BOVIN
ID TF_BOVIN STANDARD; PRT; 292 AA.
AC P30931;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Tissue factor precursor (TF) (Coagulation factor III).
GN F3.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Adrenal gland;
RX MEDLINE=92109720; PubMed=1764065;
RA Takayenoki Y., Muta T., Miyata T., Iwanaga S.;

```
RT   "cDNA and amino acid sequences of bovine tissue factor.";
RL   Biochem. Biophys. Res. Commun. 181:1145-1150(1991).
CC   -!- FUNCTION: INITIATES BLOOD COAGULATION BY FORMING A COMPLEX WITH
CC       CIRCULATING FACTOR VII OR VIIA. THE [TF:VIIA] COMPLEX ACTIVATES
CC       FACTORS IX OR X BY SPECIFIC LIMITED PROTOLYSIS. TF PLAYS A ROLE IN
CC       NORMAL HEMOSTASIS BY INITIATING THE CELL-SURFACE ASSEMBLY AND
CC       PROPAGATION OF THE COAGULATION PROTEASE CASCADE.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: BELONGS TO THE TISSUE FACTOR FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; S74147; AAB20755.1; -.
DR   PIR; JQ1319; KFBO3.
DR   HSSP; P24055; 1A21.
DR   InterPro; IPR000282; Cytok_receptor_2.
DR   InterPro; IPR001187; Tissue_factor.
DR   Pfam; PF01108; Tissue_fac; 1.
DR   PRINTS; PR00346; TISSUEFACTOR.
DR   PROSITE; PS00621; TISSUE_FACTOR; 1.
KW   Glycoprotein; Blood coagulation; Transmembrane; Signal; Lipoprotein;
KW   Palmitate.
FT   SIGNAL        1     35
FT   CHAIN        36    292       TISSUE FACTOR.
FT   DOMAIN       36    248       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    249    271       POTENTIAL.
FT   DOMAIN      272    292       CYTOPLASMIC (POTENTIAL).
FT   SITE         46     48       WKS MOTIF.
FT   CARBOHYD     43     43       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    153    153       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    181    181       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   DISULFID     81     89       BY SIMILARITY.
FT   DISULFID    215    238       BY SIMILARITY.
FT   LIPID       274    274       PALMITATE (BY SIMILARITY).
SQ   SEQUENCE   292 AA;  32475 MW;  5E471D92BFBCE163 CRC64;

  Query Match             9.7%;  Score 138.5;  DB 1;  Length 292;
  Best Local Similarity   22.6%;  Pred. No. 1.9e-05;
  Matches   59;  Conservative   43;  Mismatches  104;  Indels   55;  Gaps   12;

Qy      10 LISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVYFVQYKIMFSC 69
           |    |   ||   | : :    : ::| ||  ||:|:|       : || ||
Db      21 LFGLVLIQGAGVAGTTDVVVAYNITWKSTNFKTILEWEPKPI----NHVYTVQIS----- 71

Qy      70 SMKSSHQKPSGCWQHISCNFPGCRTLAKYGQRQWKNKEDCWGTQELSCDLTSE-TSDIQE 128
                                    : |   ||||  |: |    ||:| |   :::|
Db      72 --------------------------PRLG--NWKNK--CFYTTNTECDVTDEIVKNVRE 101

Qy     129 PYYGRVRAASAGSYSE-----WSMTPRFTPWWETKI-DPPVMNITQVNGSLLVILHAPNL 182
           |  || :  | : |       :: :| |||: || :  | : :  ||   | | :
Db     102 TYLARVLSYPADTSSSTVEPPFTNSPEFTPYLETNLGQPTIQSFEQVGTKLNVTVQDART 161

Qy     183 PYRYQKEKNVSIEDYY--ELLYRVFIINNSLEKEQKVYEGAHR-AVEIEALTPHSSYC-- 237
             |      :|: | :  :| | ::    |   ::|     :   :::: :||
Db     162 LVR-ANSAFLSLRDVFGKDLNYTLYYWKASSTGKKKATTNTNGFLIDVD---KGENYCFH 217

Qy     238 VVAEIYQPMLDRRSQRSEERC 258
           | | |    ::::|  |  :|
Db     218 VQAVILSRRVNQKSPESPIKC 238


RESULT 8
TF_CAVPO
ID   TF_CAVPO       STANDARD;      PRT;   289 AA.
AC   Q9JLU8;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Tissue factor precursor (TF) (Coagulation factor III).
GN   F3.
OS   Cavia porcellus (Guinea pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX   NCBI_TaxID=10141;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RX   MEDLINE=20206020; PubMed=10744153;
RA   Shi R.J., Li W.Z., Marder V.J., Sporn L.A.;
RT   "Cloning of guinea pig tissue factor cDNA: comparison of primary
RT   structure among six mammalian species.";
RL   Thromb. Haemost. 83:455-461(2000).
CC   -!- FUNCTION: INITIATES BLOOD COAGULATION BY FORMING A COMPLEX WITH
CC       CIRCULATING FACTOR VII OR VIIA. THE [TF:VIIA] COMPLEX ACTIVATES
CC       FACTORS IX OR X BY SPECIFIC LIMITED PROTOLYSIS. TF PLAYS A ROLE IN
CC       NORMAL HEMOSTASIS BY INITIATING THE CELL-SURFACE ASSEMBLY AND
CC       PROPAGATION OF THE COAGULATION PROTEASE CASCADE.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: BELONGS TO THE TISSUE FACTOR FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF131949; AAF36523.1; -.
DR   HSSP; P13726; 1TFH.
DR   InterPro; IPR000282; Cytok_receptor_2.
DR   InterPro; IPR001187; Tissue_factor.
DR   Pfam; PF01108; Tissue_fac; 1.
DR   PRINTS; PR00346; TISSUEFACTOR.
DR   PROSITE; PS00621; TISSUE_FACTOR; FALSE_NEG.
KW   Glycoprotein; Blood coagulation; Transmembrane; Signal; Lipoprotein;
KW   Palmitate.
FT   SIGNAL        1     32       BY SIMILARITY.
FT   CHAIN        33    289       TISSUE FACTOR.
FT   DOMAIN       33    247       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    248    268       POTENTIAL.
FT   DOMAIN      269    289       CYTOPLASMIC (POTENTIAL).
FT   SITE         44     46       WKS MOTIF.
FT   SITE         75     77       WKS MOTIF.
FT   CARBOHYD     41     41       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    111    111       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    151    151       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    164    164       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   DISULFID     79     87       BY SIMILARITY.
FT   DISULFID    213    236       BY SIMILARITY.
FT   LIPID       271    271       PALMITATE (BY SIMILARITY).
SQ   SEQUENCE   289 AA;  32456 MW;  7AB97F8F58199FB1 CRC64;

  Query Match             9.6%;  Score 136.5;  DB 1;  Length 289;
  Best Local Similarity   24.9%;  Pred. No. 2.9e-05;
  Matches   50;  Conservative   32;  Mismatches   52;  Indels   67;  Gaps   11;

Qy      10 LISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVYFVQYKIMFSC 69
           |: : |  ||| :     :||  : ::| ||  ||:|:|       ::|| ||     |
Db      21 LLGWVLVQVAGAEGI--PVKPYNLTWKSTNFKTILEWEPKPI----NNVYTVQ----IST 70

Qy      70 SMKSSHQKPSGCWQHISCNFPGCRTLAKYGQRQWKNKEDCWGTQELSCDLTSETS-DIQE 128
           :::         |: |                       |:      ||||| : ::|:
Db      71 ALED--------WKSI----------------------CFSITATECDLTSEMAPNVQQ 99

Qy     129 PYYGRVRAA---SAGSYSE--WSMTPRFTPWWETKIDPP----------VMNIT------ 167
             |  || :    | |   :  :| :| |||: || :  |           :|:|
Db     100 TYLARVISLLPNSTGFLEDAVYSNSPEFTPYQETNLGQPKIESFKLVGTKLNVTVRDTQT 159

Qy     168 --QVNGSLLVI--LHAPNLPY 184
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          : ||: | :  :   || |
Db    160 LARSNGTFLSLRDIFGKNLQY 180


RESULT 9
INR1_HUMAN
ID   INR1_HUMAN     STANDARD;      PRT;   557 AA.
AC   P17181;
DT   01-AUG-1990 (Rel. 15, Created)
DT   01-AUG-1990 (Rel. 15, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Interferon-alpha/beta receptor alpha chain precursor (IFN-alpha-REC).
GN   IFNAR1 OR IFNAR.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=90124632; PubMed=2153461;
RA   Uze G., Lutfalla G., Gresser I.;
RT   "Genetic transfer of a functional human interferon alpha receptor
RT   into mouse cells: cloning and expression of its cDNA.";
RL   Cell 60:225-234(1990).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92129376; PubMed=1370833;
RA   Lutfalla G., Gardiner K., Proudhon D., Vielh E., Uze G.;
RT   "The structure of the human interferon alpha/beta receptor gene.";
RL   J. Biol. Chem. 267:2802-2809(1992).
RN   [3]
RP   PHOSPHORYLATION BY TYK2.
RX   MEDLINE=95059042; PubMed=7526154;
RA   Colamonici O., Yan H., Domanski P., Handa R., Smalley D.,
RA   Mullersman J., Witte M., Krishnan K., Krolewski J.;
RT   "Direct binding to and tyrosine phosphorylation of the alpha subunit
RT   of the type I interferon receptor by p135tyk2 tyrosine kinase.";
RL   Mol. Cell. Biol. 14:8133-8142(1994).
CC   -!- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPE
CC       I IFNS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS
CC       INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA-AND BETA-
CC       SUBUNITS THEMSELVES.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- TISSUE SPECIFICITY: IFN RECEPTORS ARE PRESENT IN ALL TISSUES AND
CC       EVEN ON THE SURFACE OF MOST IFN-RESISTANT CELLS.
CC   -!- PTM: PHOSPHORYLATED ON TYROSINE RESIDUES BY TYK2 TYROSINE KINASE.
CC   -!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC   -!- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; J03171; AAA52730.1; -.
DR   EMBL; X60459; CAA42992.1; -.
DR   PIR; A32694; A32694.
DR   PIR; S17112; S17112.
DR   Genew; HGNC:5432; IFNAR1.
DR   MIM; 107450; -.
DR   InterPro; IPR000282; Cytok_receptor_2.
KW   Receptor; Transmembrane; Glycoprotein; Signal; Polymorphism;
KW   Phosphorylation.
FT   SIGNAL        1     27       POTENTIAL.
FT   CHAIN        28    557       INTERFERON-ALPHA/BETA RECEPTOR ALPHA
FT                                CHAIN.
FT   DOMAIN       28    436       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    437    457       POTENTIAL.
FT   DOMAIN      458    557       CYTOPLASMIC (POTENTIAL).
FT   DISULFID     79     87       BY SIMILARITY.
FT   DISULFID    199    220       BY SIMILARITY.
FT   MOD_RES     466    466       PHOSPHORYLATION (BY TYK2) (PROBABLE).
FT   MOD_RES     481    481       PHOSPHORYLATION (BY TYK2) (PROBABLE).
FT   CARBOHYD     50     50       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     58     58       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     81     81       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     88     88       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    110    110       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    172    172       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    254    254       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    313    313       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    314    314       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    376    376       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    416    416       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    433    433       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARIANT     168    168       L -> V.
FT                                /FTId=VAR_002717.
FT   CONFLICT     17     17       G -> A (IN REF. 2).
SQ   SEQUENCE   557 AA;  63525 MW;  0F6744C8A1ADBE73 CRC64;

  Query Match             9.6%;  Score 136.5;  DB 1;  Length 557;
  Best Local Similarity  20.8%;  Pred. No. 6.3e-05;
  Matches   54;  Conservative   39;  Mismatches  115;  Indels   51;  Gaps    7;

Qy       2 PKHCFLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVYFV 61
            | ||              |   :|   |: ::   :| : :|:|      |  :  : |
Db     217 PVHCI------------KTTVENELPPPENIEVSVQNQNYVLKWD----YTYANMTFQV 259

Qy      62 QYKIMFSCSMKSSHQKPSGCWQHISCNFPGCRTLAKYGQRQWKNKEDCWGTQELSCDLTS 121
           |:   |      :|                        :||   ||   :   |
Db     260 QWLHAFLKRNPGNH----------------------LYKWKQIPDCENVKTTQCVFPQ 295

Qy     122 ETSDIQEPYYGRVRAASAGSYSEWSMTPRFTPWWETKIDPPVMNITQVNGSLLVILHAPN 181
                :  | ||:|:   : | ||   :|    :  : |||  ||  :: |  : : ||
Db     296 NVFQ-KGIYLLRVQASDGNNTSFWSEEIKFDTEIQAFLLPPVFNIRSLSDSFHIYIGAP- 353

Qy     182 LPYRYQKEKNVSIEDYYELLYRVFIINNSLEKEQKVYEGAHRAVEIEALTPHSSYCVVAE 241
                ::  |  :   | |:| :    |:   |:|: |     | :  | | : |||  |
Db     354 -----KQSGNTPVIQDYPLIYEIIFWENTSNAERKIIE-KKTDVTVPNLKPLTVYCVKAR 407

Qy     242 IY--QPMLDRRSQRSEERC 258
             :     |:: |  |:  |
Db     408 AHTMDEKLNKSSVFSDAVC 426


RESULT 10
INR1_SHEEP
ID   INR1_SHEEP     STANDARD;      PRT;   560 AA.
AC   Q28589; Q95206;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Interferon-alpha/beta receptor alpha chain precursor (IFN-alpha-REC)
DE   (Interferon alpha/beta receptor-1).
GN   IFNAR1 OR IFNAR.
OS   Ovis aries (Sheep).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Caprinae; Ovis.
OX   NCBI_TaxID=9940;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Endometrium;
RX   MEDLINE=97135690; PubMed=8981227;
RA   Kaluz S., Fisher P.A., Kaluzova M., Sheldrick E.L., Flint A.P.F.;
RT   "Structure of an ovine interferon receptor and its expression in
RT   endometrium.";
RL   J. Mol. Endocrinol. 17:207-215(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Endometrium;
RX   MEDLINE=98006426; PubMed=9348203;
RA   Han C.-S., Mathialagan N., Klemann S.W., Roberts R.M.;
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RT   "Molecular cloning of ovine and bovine type I interferon receptor
RT   subunits from uteri, and endometrial expression of messenger
RT   ribonucleic acid for ovine receptors during the estrous cycle and
RT   pregnancy.";
RL   Endocrinology 138:4757-4767(1997).
CC   -!- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPE
CC       I IFNS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS
CC       INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA-AND BETA-
CC       SUBUNITS THEMSELVES.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES EXAMINED EXCEPT
CC       CONCEPTUS AT DAY 15 OF PREGNANCY.
CC   -!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC   -!- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
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CC   ---------------------------------------------------------------------
DR   EMBL; X95939; CAA65183.1; -.
DR   EMBL; U65978; AAB84231.1; -.
DR   InterPro; IPR000282; Cytok_receptor_2.
KW   Receptor; Transmembrane; Glycoprotein; Signal.
FT   SIGNAL       1     24       BY SIMILARITY.
FT   CHAIN       25    560       INTERFERON-ALPHA/BETA RECEPTOR ALPHA
FT                               CHAIN.
FT   DOMAIN      25    437       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   438    458       POTENTIAL.
FT   DOMAIN     459    560       CYTOPLASMIC (POTENTIAL).
FT   DISULFID    76     84       BY SIMILARITY.
FT   DISULFID   199    220       BY SIMILARITY.
FT   CARBOHYD    47     47       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    55     55       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    85     85       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   108    108       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   109    109       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   172    172       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   222    222       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   285    285       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   313    313       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   359    359       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   377    377       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   434    434       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT   352    352       S -> G (IN REF. 2).
FT   CONFLICT   522    522       A -> D (IN REF. 2).
SQ   SEQUENCE   560 AA;  63918 MW;  E7198A1905D4805C CRC64;

  Query Match             9.6%;  Score 136.5;  DB 1;  Length 560;
  Best Local Similarity  23.3%;  Pred. No. 6.3e-05;
  Matches   57;  Conservative   32;  Mismatches  109;  Indels   47;  Gaps    8;

Qy      21 TQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVYFVQYKIMFSCSMKSSHQKPSG 80
           |   |:   |: ||    |   :|:|         |: :  |:   |   :   |
Db     223 TTERHKVPSPENVQINVDNQAYVLKWD----YPYESTTFQAQWLRAFLKKIPGKH----- 273

Qy      81 CWQHISCNFPGCRTLAKYGQRQWKNKEDCWGTQELSC----DLTSETSDIQEPYYGRVRA 136
                        :||   :|       |    |: |        || ||||
Db     274 ------------------SNKWKQIPNCENVTTTHCVFPRDIFS-----MGIYYVRVRA 309

Qy     137 ASAGSYSEWSMTPRFTPWWETKIDPPVMNITQV-NGSLLVILHAPNLPYRYQKEKNVSIE 195
           ::    | ||    |    :  | |||:::  : : || | : |       :: :|:|:
Db     310 SNGNGTSFWSEEKEFNTEVKPIIFPPVISMKSITDDSLHVSVSAS------EESENMSVN 363

Qy     196 DYYELLYRVFIINNSLEKEQKVYEGAHRAVEIEALTPHSSYCVVAE--IYQPMLDRRSQR 253
             | |:| |    |:   |:|| |         | | : ||| |   |     :: |
Db     364 QLYPLVYEVIFWENTSNAERKVLE-KRTDFTFPNLKPLTVYCVKARALIENDRWNKGSSY 422

Qy     254 SEERC 258
           |:  |
Db     423 SDTVC 427


RESULT 11
INR1_MOUSE
ID   INR1_MOUSE     STANDARD;      PRT;   590 AA.
AC   P33896;
DT   01-FEB-1994 (Rel. 28, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Interferon-alpha/beta receptor alpha chain precursor (IFN-alpha-REC).
GN   IFNAR1 OR IFNAR OR IFAR.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92262522; PubMed=1533935;
RA   Uze G., Lutfalla G., Bandu M.T., Proudhon D., Mogensen K.E.;
RT   "Behavior of a cloned murine interferon alpha/beta receptor expressed
RT   in homospecific or heterospecific background.";
RL   Proc. Natl. Acad. Sci. U.S.A. 89:4774-4778(1992).
CC   -!- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPE
CC       I IFNS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS
CC       INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA-AND BETA-
CC       SUBUNITS THEMSELVES.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC   -!- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M89641; AAA37890.1; -.
DR   PIR; A45283; A45283.
DR   MGD; MGI:107658; Ifnar.
DR   InterPro; IPR000282; Cytok_receptor_2.
KW   Receptor; Transmembrane; Glycoprotein; Signal.
FT   SIGNAL       1     26       POTENTIAL.
FT   CHAIN       27    590       INTERFERON-ALPHA/BETA RECEPTOR ALPHA
FT                               CHAIN.
FT   DOMAIN      27    429       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   430    449       POTENTIAL.
FT   DOMAIN     450    590       CYTOPLASMIC (POTENTIAL).
FT   DISULFID    78     86       BY SIMILARITY.
FT   DISULFID   199    220       BY SIMILARITY.
FT   CARBOHYD    43     43       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   109    109       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   181    181       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   214    214       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   314    314       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   370    370       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   409    409       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   413    413       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   590 AA;  65776 MW;  7EC6DFF370185D3A CRC64;

  Query Match             9.4%;  Score 134.5;  DB 1;  Length 590;
  Best Local Similarity  21.4%;  Pred. No. 0.0001;
  Matches   45;  Conservative   39;  Mismatches   99;  Indels   27;  Gaps    7;

Qy      55 NSSVYFV--QYKIMFSCSMKSSHQKPSGCWQHISCNFPGCRTLAKY---GQRQWKNKEDC 109
           |  || :   | : :     ||| :  |     |  |      |:|    : :|    :|
Db      34 NIDVYIIDDNYTLKW-----SSHGESMG-----SVTFS-----AEYRTKDEAKWLKVPEC 78

Qy     110 WGTQELSCDLTSETSDIQEPYYGRVRAASAGSYSEWSMTPRFTPWWETKIDPPVMNITQV 169
             |    |: :   :::      ||||    | | |:    | |::   : || : :
Db      79 QHTTTTKCEFSLLDTNVYIKTQFRVRAEEGNSTSSWNEVDPFIPFYTAHMSPPEVRLEAE 138
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Qy     170 NGSLLVILHAPNLPYRYQKEKNVSIEDYYELLYRVFIINNSLEKEQKVYEGAHRAVEIEA 229
           : ::|| :  |       :: |:   :     | : |   |   ::|     :   :|
Db     139 DKAILVHISPPG------QDGNMWALEKPSFSYTIRIWQKS-SSDKKTINSTYYVEKIPE 191

Qy     230 LTPHSSYCVVAEIYQPMLDRRSQRSEERCV 259
           | | ::||:  :   | | : |  |  :|:
Db     192 LLPETTYCLEVKAIHPSLKKHSNYSTVQCI 221


RESULT 12
TF_RABIT
ID   TF_RABIT       STANDARD;      PRT;   292 AA.
AC   P24055;
DT   01-MAR-1992 (Rel. 21, Created)
DT   01-MAR-1992 (Rel. 21, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Tissue factor precursor (TF) (Coagulation factor III).
GN   F3.
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Heart;
RX   MEDLINE=91200676; PubMed=1840552;
RA   Andrews B.S., Rehemtulla A., Fowler B.J., Edgington T.S., Mackman N.;
RT   "Conservation of tissue factor primary sequence among three mammalian
RT   species.";
RL   Gene 98:265-269(1991).
RN   [2]
RP   SEQUENCE OF 33-292 FROM N.A.
RC   STRAIN=New Zealand white; TISSUE=Brain;
RX   MEDLINE=92081032; PubMed=1746002;
RA   Pawashe A., Ezekowitz M., Lin T.C., Horton R., Bach R., Konigsberg W.;
RT   "Molecular cloning, characterization and expression of cDNA for
RT   rabbit brain tissue factor.";
RL   Thromb. Haemost. 66:315-320(1991).
RN   [3]
RP   X-RAY CRYSTALLOGRAPHY (2.35 ANGSTROMS) OF 36-240.
RX   MEDLINE=98266351; PubMed=9605315;
RA   Muller Y.A., Kelley R.F., de Vos A.M.;
RT   "Hinge bending within the cytokine receptor superfamily revealed by
RT   the 2.4 A crystal structure of the extracellular domain of rabbit
RT   tissue factor.";
RL   Protein Sci. 7:1106-1115(1998).
CC   -!- FUNCTION: INITIATES BLOOD COAGULATION BY FORMING A COMPLEX WITH
CC       CIRCULATING FACTOR VII OR VIIA. THE [TF:VIIA] COMPLEX ACTIVATES
CC       FACTORS IX OR X BY SPECIFIC LIMITED PROTOLYSIS. TF PLAYS A ROLE IN
CC       NORMAL HEMOSTASIS BY INITIATING THE CELL-SURFACE ASSEMBLY AND
CC       PROPAGATION OF THE COAGULATION PROTEASE CASCADE.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- TISSUE SPECIFICITY: BRAIN, HEART.
CC   -!- SIMILARITY: BELONGS TO THE TISSUE FACTOR FAMILY.
CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; M55390; AAA63469.1; -.
DR   EMBL; X53521; CAA37597.1; -.
DR   PIR; JU0441; KFRB3.
DR   PIR; S23681; S23681.
DR   PDB; 1A21; 27-MAY-98.
DR   InterPro; IPR000282; Cytok_receptor_2.
DR   InterPro; IPR001187; Tissue_factor.
DR   Pfam; PF01108; Tissue_fac; 1.
DR   PRINTS; PR00346; TISSUEFACTOR.
DR   PROSITE; PS00621; TISSUE_FACTOR; 1.
KW   Glycoprotein; Blood coagulation; Transmembrane; Signal; Lipoprotein;
KW   Palmitate; 3D-structure.
FT   SIGNAL        1     32
FT   CHAIN        33    292       TISSUE FACTOR.
FT   DOMAIN       33    250       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    251    271       POTENTIAL.
FT   DOMAIN      272    292       CYTOPLASMIC (POTENTIAL).
FT   SITE         44     46       WKS MOTIF.
FT   SITE         75     77       WKS MOTIF.
FT   CARBOHYD     41     41       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    114    114       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    154    154       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    167    167       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    182    182       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   DISULFID     79     87
FT   DISULFID    216    239
FT   LIPID       274    274       PALMITATE (BY SIMILARITY).
SQ   SEQUENCE   292 AA;  32738 MW;  4860A1CADBACCF71 CRC64;

  Query Match             9.3%;  Score 132.5;  DB 1;  Length 292;
  Best Local Similarity   22.2%;  Pred. No. 6.7e-05;
  Matches   62;  Conservative   39;  Mismatches   89;  Indels   89;  Gaps   13;

Qy      10 LISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVYFVQYKIMFSC 69
           |: : |  ||    |  : :   : ::| ||  ||:|:|       |:  | | :  |
Db      21 LLGWLLAQVARAADT--TGRAYNLTWKSTNFKTILEWEP-------KSIDHV-YTVQIST 70

Qy      70 SMKSSHQKPSGCWQHISCNFPGCRTLAKYGQRQWKNKEDCWGTQELSCDLTSE-TSDIQE 128
             :::                                ||:|  |: | |  |||| |   |: :
Db      71 RLEN----------------------------WKSK--CFLTAETECDLTDEVVKDVGQ 99

Qy     129 PYYGRV-----RAASAGSYSE---WSMTPRFTPWWETKIDPPV----------MNITQVN 170
             |  ||     |  :   : |   :  :| |||: :| :  |           :|:|  :
Db     100 TYMARVLSYPARNGNTTGFPEEPPFRNSPEFTPYLDTNLGQPTIQSFEQVGTKLNVTVQD 159

Qy     171 GSLLVILHAPNLPYR--YQKEKNVSIEDYYELLY-------RVFIINNSLEKEQKVYEGA 221
             ||  :   |  |  : |: |       | | |       :     |: |    | :|
Db     160 ARTLVRRNGTFLSLRAVFGKDLN------YTLYYWRASSTGKKTATTNTNEFLIDVDKGE 213

Qy     222 HRAVEIEALTPHSSYCVVAEIYQPMLDRRSQRSEERCVE 260
           :   ::|: |               :| ||| |   |
Db     214 NYCFSVQAVIPSR-------------KRKQRSPESLTE 238


RESULT 13 .
TF_RAT
ID   TF_RAT         STANDARD;      PRT;   295 AA.
AC   P42533;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Tissue factor precursor (TF) (Coagulation factor III).
GN   CF3.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley;
RX   MEDLINE=97108126; PubMed=8950776;
RA   Taby O., Rosenfield C.L., Bogdanov V., Nemerson Y., Taubman M.B.;
RT   "Cloning of the rat tissue factor cDNA and promoter: identification
RT   of a serum-response region.";
RL   Thromb. Haemost. 76:697-702(1996).
CC   -!- FUNCTION: INITIATES BLOOD COAGULATION BY FORMING A COMPLEX WITH
CC       CIRCULATING FACTOR VII OR VIIA. THE [TF:VIIA] COMPLEX ACTIVATES
CC       FACTORS IX OR X BY SPECIFIC LIMITED PROTOLYSIS. TF PLAYS A ROLE IN
CC       NORMAL HEMOSTASIS BY INITIATING THE CELL-SURFACE ASSEMBLY AND
CC       PROPAGATION OF THE COAGULATION PROTEASE CASCADE.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: BELONGS TO THE TISSUE FACTOR FAMILY.
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U07619; AAA16966.1; -.
DR   HSSP; P13726; 1FAK.
DR   InterPro; IPR000282; Cytok_receptor_2.
DR   InterPro; IPR001187; Tissue_factor.
DR   Pfam; PF01108; Tissue_fac; 1.
DR   PRINTS; PR00346; TISSUEFACTOR.
DR   PROSITE; PS00621; TISSUE_FACTOR; 1.
KW   Glycoprotein; Blood coagulation; Transmembrane; Signal; Lipoprotein;
KW   Palmitate.
FT   SIGNAL        1     28       BY SIMILARITY.
FT   CHAIN        29    295       TISSUE FACTOR.
FT   DOMAIN       29    252       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    253    275       POTENTIAL.
FT   DOMAIN      276    295       CYTOPLASMIC (POTENTIAL).
FT   SITE        246    248       WKS MOTIF.
FT   CARBOHYD     38     38       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     58     58       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     95     95       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    109    109       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    170    170       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    201    201       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   DISULFID     76     84       BY SIMILARITY.
FT   DISULFID    219    242       BY SIMILARITY.
FT   LIPID       276    276       PALMITATE (BY SIMILARITY).
SQ   SEQUENCE   295 AA;  33443 MW;  EE4C15B4E3628D48 CRC64;

  Query Match             9.0%;  Score 128.5;  DB 1;  Length 295;
  Best Local Similarity  22.9%;  Pred. No. 0.00016;
  Matches   66;  Conservative   37;  Mismatches   92;  Indels   93;  Gaps   14;

Qy       6 FLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVYFVQYKI 65
           |||||:     | |||       |   : : | :|  ||:|||       :  | ||
Db      17 FLGFLLLQVAVG-AGTPPG----KAFNLTWISTDFKTILEWQP----KPTNYTYTVQ--- 64

Qy      66 MFSCSMKSSHQKPSGCWQHISCNFPGCRTLAKYGQRQWKNKEDCWGTQELSCDLTSE-TS 124
             | :|                          | || |  | || :  |||| |
Db      65 ---ISDRS--------------------------RNWKYK--CTGTTDTECDLTDEIVK 92

Qy     125 DIQEPYYGRV-----------RAASAGSYSE---WSMTPRFTPWWETKIDPPVMNITQVN 170
           |:   |  ||           :    |:: |   ::   :| |: :|||  ||:   :
Db      93 DVNWTYEARVLSVPWRNSTHGKETLFGTHGEEPPFTNARKFLPYRDTKIGQPVIQKYEQG 152

Qy     171 GSLLVILHAPNLPYRYQKEKNVSIEDYYELLYR--VFIINNSLEKEQKVYEGAHR---AV 225
           |: |                 |:::| : |: :   |:    :       |   :|   :
Db     153 GTKL----------------KVTVKDSFTLVRKNGTFLTLRQVFGNDLGYILTYRKDSST 196

Qy     226 EIEALTPHS-----------SYCVVAE--IYQPMLDRRSQRSEERCVE 260
             :  | |:           |||  |:  |:    : :|  |  :| |
Db     197 GRKTNTTHTNEFLIDVEKGVSYCFFAQAVIFSRKTNHKSPESITKCTE 244


RESULT 14
TF_MOUSE
ID   TF_MOUSE       STANDARD;      PRT;   294 AA.
AC   P20352;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-AUG-1991 (Rel. 19, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Tissue factor precursor (TF) (Coagulation factor III).
GN   F3 OR CF3 OR CF-3.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91093171; PubMed=1985911;
RA   Ranganathan G., Blatti S.P., Subramaniam M., Fass D.N., Maihle N.J.,
RA   Getz M.J.;
RT   "Cloning of murine tissue factor and regulation of gene expression by
RT   transforming growth factor type beta 1.";
RL   J. Biol. Chem. 266:496-501(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c;
RX   MEDLINE=89343974; PubMed=2761539;
RA   Hartzell S., Ryder K., Lanahan A., Lau L.F., Nathans D.;
RT   "A growth factor-responsive gene of murine BALB/c 3T3 cells encodes a
RT   protein homologous to human tissue factor.";
RL   Mol. Cell. Biol. 9:2567-2573(1989).
CC   -!- FUNCTION: INITIATES BLOOD COAGULATION BY FORMING A COMPLEX WITH
CC       CIRCULATING FACTOR VII OR VIIA. THE [TF:VIIA] COMPLEX ACTIVATES
CC       FACTORS IX OR X BY SPECIFIC LIMITED PROTOLYSIS. TF PLAYS A ROLE IN
CC       NORMAL HEMOSTASIS BY INITIATING THE CELL-SURFACE ASSEMBLY AND
CC       PROPAGATION OF THE COAGULATION PROTEASE CASCADE.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: BELONGS TO THE TISSUE FACTOR FAMILY.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M57896; AAA63400.1; -.
DR   EMBL; M26071; AAA40414.1; -.
DR   PIR; A32318; KFMS3.
DR   HSSP; P13726; 1FAK.
DR   MGD; MGI:88381; F3.
DR   InterPro; IPR000282; Cytok_receptor_2.
DR   InterPro; IPR001187; Tissue_factor.
DR   Pfam; PF01108; Tissue_fac; 1.
DR   PRINTS; PR00346; TISSUEFACTOR.
DR   PROSITE; PS00621; TISSUE_FACTOR; 1.
KW   Glycoprotein; Blood coagulation; Transmembrane; Signal; Lipoprotein;
KW   Palmitate.
FT   SIGNAL        1     28
FT   CHAIN        29    294       TISSUE FACTOR.
FT   DOMAIN       29    251       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    252    274       POTENTIAL.
FT   DOMAIN      275    294       CYTOPLASMIC (POTENTIAL).
FT   SITE        245    247       WKS MOTIF.
FT   CARBOHYD     37     37       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     57     57       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    169    169       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    200    200       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   DISULFID     75     83       BY SIMILARITY.
FT   DISULFID    218    241       BY SIMILARITY.
FT   LIPID       275    275       PALMITATE (BY SIMILARITY).
FT   CONFLICT     26     26       I -> T (IN REF. 2).
SQ   SEQUENCE   294 AA;  32935 MW;  A306101293C31FA0 CRC64;

  Query Match             8.7%;  Score 124;  DB 1;  Length 294;
  Best Local Similarity  22.7%;  Pred. No. 0.00041;
  Matches   64;  Conservative   36;  Mismatches  100;  Indels   82;  Gaps   13;

Qy       6 FLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVYFVQYKI 65
           ||| |:   : | ||       |   : : | :|  ||:|||       :  | ||
Db      17 FLGCLLLQVIAG-AGIPE-----KAFNLTWISTDFKTILEWQP----KPTNYTYTVQ--- 63

Qy      66 MFSCSMKSSHQKPSGCWQHISCNFPGCRTLAKYGQRQWKNKEDCWGTQELSCDLTSE-TS 124
             | :|                          | |||| |: | :  |||| |
Db      64 ---ISDRS--------------------------RNWKNK--CFSTTDTECDLTDEIVK 91

Qy     125 DIQEPYYGRVRAASA-------------GSYSEWSMTPRFTPWWETKIDPPV------- 163
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          |:   |  :| :                    |    ::  |:| |: :| :  ||
Db      92 DVTWAYEAKVLSVPRRNSVHGDGDQLVIHGEEPPFTNAPKFLPYRDTNLGQPVIQQFEQD 151

Qy     164 ---MNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYYELLYRVFIINNSLEKEQKVYEG 220
           :|:   :   ||  :   |  |    |::     | : ||     :|  |:  :
Db     152 GRKLNVVVKDSLTLVRKNGTFLTLRQVFGKDLG----YIITYRK---GSSTGKKTNITNT 204

Qy     221 AHRAVEIEALTPHSSYC--VVAEIYQPMLDRRSQRSEERCVE 260
           ::::|      |||  | | |:    :: |  |   | |
Db     205 NEFSIDVE---EGVSYCFFVQAMIFSRKTNQNSPGSSTVCTE 243


RESULT 15
INGR_HUMAN
ID   INGR_HUMAN     STANDARD;      PRT;   489 AA.
AC   P15260;
DT   01-APR-1990 (Rel. 14, Created)
DT   01-APR-1990 (Rel. 14, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Interferon-gamma receptor alpha chain precursor (CDw119).
GN   IFNGR1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89003065; PubMed=2971451;
RA   Aguet M., Dembic Z., Merlin G.;
RT   "Molecular cloning and expression of the human interferon-gamma
RT   receptor.";
RL   Cell 55:273-280(1988).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Phillimore B.;
RL   Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Prostate;
RA   Strausberg R.;
RL   Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   DISULFIDE BONDS, PARTIAL SEQUENCE, AND MUTAGENESIS.
RX   MEDLINE=93183911; PubMed=8443182;
RA   Stueber D., Friedlein A., Fountoulakis M., Lahm H.-W., Garotta G.;
RT   "Alignment of disulfide bonds of the extracellular domain of the
RT   interferon gamma receptor and investigation of their role in
RT   biological activity.";
RL   Biochemistry 32:2423-2430(1993).
RN   [5]
RP   X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 26-248.
RX   MEDLINE=95342235; PubMed=7617032;
RA   Walter M.R., Windsor W.T., Nagabhushan T.L., Lundell D.J., Lunn C.A.,
RA   Zauodny P.J., Narula S.K.;
RT   "Crystal structure of a complex between interferon-gamma and its
RT   soluble high-affinity receptor.";
RL   Nature 376:230-235(1995).
RN   [6]
RP   X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 28-122 IN COMPLEX WITH
RP   ANTIBODY.
RX   MEDLINE=98035727; PubMed=9367779;
RA   Sogabe S., Stuart F., Henke C., Bridges A., Williams G., Birch A.,
RA   Winkler F.K., Robinson J.A.;
RT   "Neutralizing epitopes on the extracellular interferon gamma receptor
RT   (IFNgammaR) alpha-chain characterized by homolog scanning mutagenesis
RT   and X-ray crystal structure of the A6 fab-IFNgammaR1-108 complex.";
RL   J. Mol. Biol. 273:882-897(1997).
RN   [7]
RP   X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF COMPLEX WITH ING.
RX   MEDLINE=20444407; PubMed=10986460;
RA   Thiel D.J., le Du M.-H., Walter R.L., D'Arcy A., Chene C.,
RA   Fountoulakis M., Garotta G., Winkler F.K., Ealick S.E.;
RT   "Observation of an unexpected third receptor molecule in the crystal
RT   structure of human interferon-gamma receptor complex.";
RL   Structure 8:927-936(2000).
CC   -!- FUNCTION: RECEPTOR FOR INTERFERON GAMMA. TWO RECEPTORS BIND ONE
CC       INTERFERON-GAMMA DIMER.
CC   -!- SUBUNIT: MONOMER.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- PTM: PHOSPHORYLATED AT SER/THR RESIDUES.
CC   -!- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC   -!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC   -!- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
CC   -!- DATABASE: NAME=PROW; NOTE=CD guide CDw119 entry;
CC       WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cdw119.htm".
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; J03143; AAA52731.1; -.
DR   EMBL; AL050337; CAB53062.1; -.
DR   EMBL; BC005333; AAH05333.1; -.
DR   PIR; A31555; A31555.
DR   PDB; 1JRH; 25-MAR-98.
DR   PDB; 1FG9; 11-AUG-00.
DR   GlycoSuiteDB; P15260; -.
DR   Genew; HGNC:5439; IFNGR1.
DR   MIM; 107470; -.
DR   MIM; 209950; -.
DR   InterPro; IPR000282; Cytok_receptor_2.
KW   Receptor; Transmembrane; Glycoprotein; Signal; Phosphorylation;
KW   Immunoglobulin domain; 3D-structure.
FT   SIGNAL        1     17
FT   CHAIN        18    489       INTERFERON-GAMMA RECEPTOR ALPHA CHAIN.
FT   DOMAIN       18    245       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    246    266       POTENTIAL.
FT   DOMAIN      267    489       CYTOPLASMIC (POTENTIAL).
FT   DISULFID     77     85
FT   DISULFID    122    167
FT   DISULFID    195    200
FT   DISULFID    214    235
FT   CARBOHYD     34     34       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     79     79       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     86     86       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    179    179       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    240    240       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   489 AA;  54404 MW;  DCF9E574D8F47400 CRC64;

  Query Match             8.6%;  Score 122.5;  DB 1;  Length 489;
  Best Local Similarity   20.1%;  Pred. No. 0.001;
  Matches   56;  Conservative   49;  Mismatches  103;  Indels   71;  Gaps   10;

Qy       9 FLISFFLTGVA----GTQSTHESL--KPQRVQFQSRNFHNILQWQPGRALTGNSSVYFVQ 62
           ||:   : ||:    ||     |    |  |  :| | : |: |             :
Db       5 FLLPLVMQGVSRAEMGTADLGPSSVPTPTNVTIESYNMNPIVYW--------------E 49

Qy      63 YKIM-----FSCSMKSSHQKPSGCWQHISCNFPGCRTLAKYGQRQWKNKEDCWGTQELSC 117
           |:||     |:  :|:                          || :  :  : |      |
Db      50 YQIMPQVPVFTVEVKN----------------------YGVKNSEWIDACINISHHYC 85

Qy     118 DLTSETSDIQEPYYGRVRAASAGSYSEWSMTPRFTPWWETKIDPPVMNITQVNGSLLVIL 177
           :::    |    : ||:|     | ::  :  |    : || || ::| :    ::: :
Db      86 NISDHVGDPSNSLWVRVKARVGQKESAYAKSEEFAVCRDGKIGPPKLDIRKEEKQIMIDI 145

Qy     178 HAPNLPYRYQKEKNVSIEDY------YELLYRVFIINNSLEKEQKVYE---------GAH 222
           |:: :   |: |   ||      |  :| |::  |  | : |:
Db     146 FHPSV-FVNGDEQEV---DYDPETTCYIRVYNVYVRMNGSEIQYKILTQKEDDCDEIQCQ 201

Qy     223 RAVEIEALTPHSSYCVVAEIYQPMLDRRSQRSEERCVEI 261
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Db     202 LAIPVSSL--NSQYCVSAEGVLHVWGVTTEKSKEVCITI 238
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Search completed: December 22, 2002, 10:11:37
Job time : 28 secs

GenCore version 5.1.3

OM protein - protein search, using sw model

Run on: December 22, 2002, 10:09:37 ; Search time 26 Seconds
(without alignments)
296.493 Million cell updates/sec

Title: US-09-964-994-2
Perfect score: 1427
Sequence: 1 MPKHCFLGFLISFFLTGVAG.....YQPMLDRRSQRSEERCVEIP 262

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	311	21.8	221	2	US-08-943-087-52	Sequence 52, Appl
2	310	21.7	221	2	US-08-943-087-50	Sequence 50, Appl
3	310	21.7	221	2	US-08-943-087-56	Sequence 56, Appl
4	310	21.7	553	2	US-08-943-087-2	Sequence 2, Appli
5	310	21.7	553	2	US-08-943-087-14	Sequence 14, Appl
6	310	21.7	553	2	US-08-943-087-16	Sequence 16, Appl
7	310	21.7	553	2	US-08-943-087-18	Sequence 18, Appl
8	310	21.7	553	2	US-08-943-087-20	Sequence 20, Appl
9	310	21.7	553	2	US-08-943-087-22	Sequence 22, Appl
10	310	21.7	553	2	US-08-943-087-24	Sequence 24, Appl
11	310	21.7	553	2	US-08-943-087-26	Sequence 26, Appl
12	310	21.7	553	2	US-08-943-087-28	Sequence 28, Appl
13	310	21.7	553	2	US-08-943-087-30	Sequence 30, Appl
14	310	21.7	553	2	US-08-943-087-32	Sequence 32, Appl
15	310	21.7	553	2	US-08-943-087-34	Sequence 34, Appl
16	310	21.7	553	2	US-08-943-087-36	Sequence 36, Appl
17	310	21.7	553	2	US-08-943-087-38	Sequence 38, Appl
18	310	21.7	553	2	US-08-943-087-40	Sequence 40, Appl
19	310	21.7	553	2	US-08-943-087-42	Sequence 42, Appl
20	310	21.7	553	2	US-08-943-087-44	Sequence 44, Appl
21	310	21.7	553	2	US-08-943-087-46	Sequence 46, Appl
22	310	21.7	553	2	US-08-943-087-48	Sequence 48, Appl
23	308	21.6	221	2	US-08-943-087-54	Sequence 54, Appl
24	303	21.2	221	2	US-08-943-087-58	Sequence 58, Appl
25	299	21.0	221	2	US-08-943-087-60	Sequence 60, Appl
26	240	16.8	574	2	US-08-906-713-2	Sequence 2, Appli
27	164.5	11.5	575	1	US-08-424-788-2	Sequence 2, Appli
28	164.5	11.5	575	1	US-08-110-683-4	Sequence 4, Appli
29	164.5	11.5	575	2	US-08-477-166-4	Sequence 4, Appli
30	164.5	11.5	575	2	US-08-472-097-4	Sequence 4, Appli
31	164.5	11.5	575	4	US-09-439-672-4	Sequence 4, Appli
32	164.5	11.5	575	5	PCT-US93-11638-4	Sequence 4, Appli
33	163	11.4	251	1	US-07-882-202A-2	Sequence 2, Appli
34	163	11.4	251	1	US-07-683-682B-4	Sequence 4, Appli
35	163	11.4	251	1	US-08-021-615A-2	Sequence 2, Appli
36	163	11.4	251	1	US-08-321-777-2	Sequence 2, Appli
37	163	11.4	251	1	US-08-463-931-6	Sequence 6, Appli
38	163	11.4	251	1	US-08-464-237A-4	Sequence 4, Appli
39	163	11.4	251	5	PCT-US92-02898A-4	Sequence 4, Appli
40	163	11.4	251	5	PCT-US93-04493-2	Sequence 2, Appli
41	163	11.4	295	1	US-08-463-931-2	Sequence 2, Appli
42	163	11.4	295	2	US-08-372-887-20	Sequence 20, Appl
43	163	11.4	295	4	US-09-224-048A-4	Sequence 4, Appli
44	162	11.4	559	1	US-08-424-788-3	Sequence 3, Appli
45	155	10.9	227	4	US-08-871-572B-14	Sequence 14, Appl

ALIGNMENTS

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RESULT 1
US-08-943-087-52
; Sequence 52, Application US/08943087
; Patent No. 5945511
;  GENERAL INFORMATION:
;    APPLICANT:  Lok, Si
;    APPLICANT:  Kho, Choon J.
;    APPLICANT:  Jelmberg, Anna C.
;    APPLICANT:  Adams, Robyn L.
;    APPLICANT:  Whitmore, Theodore E.
;    APPLICANT:  Farrah, Theresa M.
;    TITLE OF INVENTION:  CYTOKINE RECEPTOR
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ZymoGenetics, Inc.
;      STREET:  1201 Eastlake Avenue East
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98102
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/943,087
;      FILING DATE:
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/803,305
;      FILING DATE:  20-FEB-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lunn, Paul G
;      REGISTRATION NUMBER:  32,743
;      REFERENCE/DOCKET NUMBER:  96-24C1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206-442-6627
;      TELEFAX:  206-442-6678
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  52:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  221 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FRAGMENT TYPE:  internal
US-08-943-087-52
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  Best Local Similarity   32.0%;  Pred. No. 1.3e-27;
  Matches   74;  Conservative   33;  Mismatches   90;  Indels   34;  Gaps    3;

Qy      29 KPQRVQFQSRNFHNILQWQPGRALTGNSSVYFVQYKIMFSCSMKSSHQKPSGCWQHISCN 88
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Qy      89 FPGCRTLAKYGQRQWKNKEDCWGTQELSCDLTSETSDIQEPYYGRVRAASAGSYSEWSMT 148
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Qy     149 PRFTPWWETKIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYY-ELLYRVFII 207
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Qy     208 NNSLEKEQKVYEGAHRAVEIEALTPHSSYCVVAEIYQPMLDRRSQRSEERC 258
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ULT 2
US-08-943-087-50
; Sequence 50, Application US/08943087
; Patent No. 5945511
;  GENERAL INFORMATION:
;    APPLICANT:  Lok, Si
;    APPLICANT:  Kho, Choon J.
;    APPLICANT:  Jelmberg, Anna C.
;    APPLICANT:  Adams, Robyn L.
;    APPLICANT:  Whitmore, Theodore E.
;    APPLICANT:  Farrah, Theresa M.
;    TITLE OF INVENTION:  CYTOKINE RECEPTOR
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ZymoGenetics, Inc.
;      STREET:  1201 Eastlake Avenue East
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98102
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/943,087
;      FILING DATE:
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/803,305
;      FILING DATE:  20-FEB-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lunn, Paul G
;      REGISTRATION NUMBER:  32,743
;      REFERENCE/DOCKET NUMBER:  96-24C1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206-442-6627
;      TELEFAX:  206-442-6678
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  50:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  221 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FRAGMENT TYPE:  internal
US-08-943-087-50
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  Query Match             21.7%;  Score 310;  DB 2;  Length 221;
  Best Local Similarity   32.0%;  Pred. No. 1.7e-27;
  Matches   74;  Conservative   33;  Mismatches   90;  Indels   34;  Gaps    3;

Qy      29 KPQRVQFQSRNFHNILQWQPGRALTGNSSVYFVQYKIMFSCSMKSSHQKPSGCWQHISCN 88
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Qy      89 FPGCRTLAKYGQRQWKNKEDCWGTQELSCDLTSETSDIQEPYYGRVRAASAGSYSEWSMT 148
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Qy     149 PRFTPWWETKIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYY-ELLYRVFII 207
            || |: ||:| || : :|    |: |:| ||    |  ::  ||::  |  | | | ::
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Qy     208 NNSLEKEQKVYEGAHRAVEIEALTPHSSYCVVAEIYQPMLDRRSQRSEERC 258
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RESULT 3
US-08-943-087-56
; Sequence 56, Application US/08943087
; Patent No. 5945511
;  GENERAL INFORMATION:
;    APPLICANT:  Lok, Si
;    APPLICANT:  Kho, Choon J.
;    APPLICANT:  Jelmberg, Anna C.
;    APPLICANT:  Adams, Robyn L.
;    APPLICANT:  Whitmore, Theodore E.
;    APPLICANT:  Farrah, Theresa M.
;    TITLE OF INVENTION:  CYTOKINE RECEPTOR
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ZymoGenetics, Inc.
;      STREET:  1201 Eastlake Avenue East
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98102
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/943,087
;      FILING DATE:
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/803,305
;      FILING DATE:  20-FEB-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lunn, Paul G
;      REGISTRATION NUMBER:  32,743
;      REFERENCE/DOCKET NUMBER:  96-24C1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206-442-6627
;      TELEFAX:  206-442-6678
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  56:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  221 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FRAGMENT TYPE:  internal
US-08-943-087-56
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  Query Match             21.7%;  Score 310;  DB 2;  Length 221;
  Best Local Similarity   31.6%;  Pred. No. 1.7e-27;
  Matches   73;  Conservative   34;  Mismatches   90;  Indels   34;  Gaps    3;
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Qy      89 FPGCRTLAKYGQRQWKNKEDCWGTQELSCDLTSETSDIQEPYYGRVRAASAGSYSEWSMT 148
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Db      47 ---------YGQKKWLNKSECRNINRTYCDLSAETSDYEHQYYAKVKAIWGSKCSKWAES 97

Qy     149 PRFTPWWETKIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYY-ELLYRVFII 207
            || |: |::| || : :|    |: |:| ||    |  ::  ||::  |  | | | ::
Db      98 GRFYPFLESQIGPPEVALTSDEKSISVVLSAPEKWKRNPEDLPVSMQQIYSNLKYNVSVL 157

Qy     208 NNSLEKEQKVYEGAHRAVEIEALTPHSSYCVVAEIYQPMLDRRSQRSEERC 258
           |    :        |  | :  | |:: |||  | : |   ||:| ||::|
Db     158 NTKSNRTWSQCVTNHTLV-LTWLEPNTLYCVHVESFVPGPPRRAQPSEKQC 207


RESULT 4
US-08-943-087-2
; Sequence 2, Application US/08943087
; Patent No. 5945511
; GENERAL INFORMATION:
;    APPLICANT:  Lok, Si
;    APPLICANT:  Kho, Choon J.
;    APPLICANT:  Jelmberg, Anna C.
;    APPLICANT:  Adams, Robyn L.
;    APPLICANT:  Whitmore, Theodore E.
;    APPLICANT:  Farrah, Theresa M.
;    TITLE OF INVENTION:  CYTOKINE RECEPTOR
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ZymoGenetics, Inc.
;      STREET:  1201 Eastlake Avenue East
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98102
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/943,087
;      FILING DATE:
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/803,305
;      FILING DATE:  20-FEB-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lunn, Paul G
;      REGISTRATION NUMBER:  32,743
;      REFERENCE/DOCKET NUMBER:  96-24C1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206-442-6627
;      TELEFAX:  206-442-6678
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  553 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FRAGMENT TYPE:  internal
US-08-943-087-2

  Query Match             21.7%;  Score 310;  DB 2;  Length 553;
  Best Local Similarity   32.0%;  Pred. No. 7.2e-27;
  Matches   74;  Conservative   33;  Mismatches   90;  Indels   34;  Gaps    3;

Qy      29 KPQRVQFQSRNFHNILQWQPGRALTGNSSVYFVQYKIMFSCSMKSSHQKPSGCWQHISCN 88
           ||  : | | |  |:||| |   | |    | ||| |
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Db      39 KPANITFLSINMKNVLQWTPPEGLQGVKVTYTVQYFI---------------------- 75

Qy      89 FPGCRTLAKYGQRQWKNKEDCWGTQELSCDLTSETSDIQEPYYGRVRAASAGSYSEWSMT 148
                  |||::| || :|       |||::|||| :  || :|:|      |:|: :
Db      76 ---------YGQKKWLNKSECRNINRTYCDLSAETSDYEHQYYAKVKAIWGTKCSKWAES 126

Qy     149 PRFTPWWETKIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYY-ELLYRVFII 207
            || |: ||:| || : :|    |: |:| ||    |  ::  ||::  |  | | | ::
Db     127 GRFYPFLETQIGPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQQIYSNLKYNVSVL 186

Qy     208 NNSLEKEQKVYEGAHRAVEIEALTPHSSYCVVAEIYQPMLDRRSQRSEERC 258
           |    :        |  | :  | |:: |||  | : |   ||:| ||::|
Db     187 NTKSNRTWSQCVTNHTLV-LTWLEPNTLYCVHVESFVPGPPRRAQPSEKQC 236


RESULT 5
US-08-943-087-14
; Sequence 14, Application US/08943087
; Patent No. 5945511
; GENERAL INFORMATION:
;    APPLICANT:  Lok, Si
;    APPLICANT:  Kho, Choon J.
;    APPLICANT:  Jelmberg, Anna C.
;    APPLICANT:  Adams, Robyn L.
;    APPLICANT:  Whitmore, Theodore E.
;    APPLICANT:  Farrah, Theresa M.
;    TITLE OF INVENTION:  CYTOKINE RECEPTOR
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ZymoGenetics, Inc.
;      STREET:  1201 Eastlake Avenue East
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98102
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/943,087
;      FILING DATE:
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/803,305
;      FILING DATE:  20-FEB-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lunn, Paul G
;      REGISTRATION NUMBER:  32,743
;      REFERENCE/DOCKET NUMBER:  96-24C1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206-442-6627
;      TELEFAX:  206-442-6678
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  553 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FRAGMENT TYPE:  internal
US-08-943-087-14

  Query Match             21.7%;  Score 310;  DB 2;  Length 553;
  Best Local Similarity   32.0%;  Pred. No. 7.2e-27;
  Matches   74;  Conservative   33;  Mismatches   90;  Indels   34;  Gaps    3;

Qy      29 KPQRVQFQSRNFHNILQWQPGRALTGNSSVYFVQYKIMFSCSMKSSHQKPSGCWQHISCN 88
           ||  : | | |  |:||| |   | |    | ||| |
Db      39 KPANITFLSINMKNVLQWTPPEGLQGVKVTYTVQYFI---------------------- 75
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```
Qy      89 FPGCRTLAKYGQRQWKNKEDCWGTQELSCDLTSETSDIQEPYYGRVRAASAGSYSEWSMT 148
                  |||::| || :|       |||::|||| :  || :|:|      |:|: :
Db      76 ---------YGQKKWLNKSECRNINRTYCDLSAETSDYEHQYYAKVKAIWGTKCSKWAES 126

Qy     149 PRFTPWWETKIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYY-ELLYRVFII 207
           || |: ||:| || : :|    |: |:| ||    |  ::  ||::  |  | | | ::
Db     127 GRFYPFLETQIGPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQQIYSNLKYNVSVL 186

Qy     208 NNSLEKEQKVYEGAHRAVEIEALTPHSSYCVVAEIYQPMLDRRSQRSEERC 258
           |    :        |  | :  | |:: |||  | : |   ||:| ||::|
Db     187 NTKSNRTWSQCVTNHTLV-LTWLEPNTLYCVHVESFVPGPPRRAQPSEKQC 236
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RESULT 6
US-08-943-087-16
; Sequence 16, Application US/08943087
; Patent No. 5945511
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Farrah, Theresa M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,087
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/803,305
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-24C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-943-087-16

Query Match 21.7%; Score 310; DB 2; Length 553;
Best Local Similarity 32.0%; Pred. No. 7.2e-27;
Matches 74; Conservative 33; Mismatches 90; Indels 34; Gaps 3;

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Qy      29 KPQRVQFQSRNFHNILQWQPGRALTGNSSVYFVQYKIMFSCSMKSSHQKPSGCWQHISCN 88
           ||  : | | |  |:||| |   | |    | ||| |
Db      39 KPANITFLSINMKNVLQWTPPEGLQGVKVTYTVQYFI---------------------- 75

Qy      89 FPGCRTLAKYGQRQWKNKEDCWGTQELSCDLTSETSDIQEPYYGRVRAASAGSYSEWSMT 148
                  |||::| || :|       |||::|||| :  || :|:|      |:|: :
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Db      76 ---------YGQKKWLNKSECRNINRTYCDLSAETSDYEHQYYAKVKAIWGTKCSKWAES 126

Qy     149 PRFTPWWETKIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYY-ELLYRVFII 207
           || |: ||:| || : :|    |: |:| ||    |  ::  ||::  |  | | | ::
Db     127 GRFYPFLETQIGPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQQIYSNLKYNVSVL 186

Qy     208 NNSLEKEQKVYEGAHRAVEIEALTPHSSYCVVAEIYQPMLDRRSQRSEERC 258
           |    :        |  | :  | |:: |||  | : |   ||:| ||::|
Db     187 NTKSNRTWSQCVTNHTLV-LTWLEPNTLYCVHVESFVPGPPRRAQPSEKQC 236
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RESULT 7
US-08-943-087-18
; Sequence 18, Application US/08943087
; Patent No. 5945511
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Farrah, Theresa M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,087
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/803,305
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-24C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-943-087-18

Query Match 21.7%; Score 310; DB 2; Length 553;
Best Local Similarity 32.0%; Pred. No. 7.2e-27;
Matches 74; Conservative 33; Mismatches 90; Indels 34; Gaps 3;

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Qy      29 KPQRVQFQSRNFHNILQWQPGRALTGNSSVYFVQYKIMFSCSMKSSHQKPSGCWQHISCN 88
           ||  : | | |  |:||| |   | |    | ||| |
Db      39 KPANITFLSINMKNVLQWTPPEGLQGVKVTYTVQYFI---------------------- 75

Qy      89 FPGCRTLAKYGQRQWKNKEDCWGTQELSCDLTSETSDIQEPYYGRVRAASAGSYSEWSMT 148
                  |||::| || :|       |||::|||| :  || :|:|      |:|: :
Db      76 ---------YGQKKWLNKSECRNINRTYCDLSAETSDYEHQYYAKVKAIWGTKCSKWAES 126
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```
Qy     149 PRFTPWWETKIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYY-ELLYRVFII 207
           || |: ||:| || : :|    |: |:| ||    |  ::  ||::  |  | | | ::
Db     127 GRFYPFLETQIGPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQQIYSNLKYNVSVL 186

Qy     208 NNSLEKEQKVYEGAHRAVEIEALTPHSSYCVVAEIYQPMLDRRSQRSEERC 258
           |    :        |  | :  | |:: |||  | : |   ||:| ||::|
Db     187 NTKSNRTWSQCVTNHTLV-LTWLEPNTLYCVHVESFVPGPPRRAQPSEKQC 236


RESULT 8
US-08-943-087-20
; Sequence 20, Application US/08943087
; Patent No. 5945511
;  GENERAL INFORMATION:
;    APPLICANT:  Lok, Si
;    APPLICANT:  Kho, Choon J.
;    APPLICANT:  Jelmberg, Anna C.
;    APPLICANT:  Adams, Robyn L.
;    APPLICANT:  Whitmore, Theodore E.
;    APPLICANT:  Farrah, Theresa M.
;    TITLE OF INVENTION:  CYTOKINE RECEPTOR
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ZymoGenetics, Inc.
;      STREET:  1201 Eastlake Avenue East
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98102
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/943,087
;      FILING DATE:
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/803,305
;      FILING DATE:  20-FEB-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lunn, Paul G
;      REGISTRATION NUMBER:  32,743
;      REFERENCE/DOCKET NUMBER:  96-24C1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206-442-6627
;      TELEFAX:  206-442-6678
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  553 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FRAGMENT TYPE:  internal
US-08-943-087-20

  Query Match             21.7%;  Score 310;  DB 2;  Length 553;
  Best Local Similarity   32.0%;  Pred. No. 7.2e-27;
  Matches   74;  Conservative   33;  Mismatches   90;  Indels   34;  Gaps    3;

Qy      29 KPQRVQFQSRNFHNILQWQPGRALTGNSSVYFVQYKIMFSCSMKSSHQKPSGCWQHISCN 88
           ||  : | | |  |:||| |   | |    | ||| |
Db      39 KPANITFLSINMKNVLQWTPPEGLQGVKVTYTVQYFI---------------------- 75

Qy      89 FPGCRTLAKYGQRQWKNKEDCWGTQELSCDLTSETSDIQEPYYGRVRAASAGSYSEWSMT 148
                 |||::| || :|       |||::|||| :  || :|:|      |:|: :
Db      76 ---------YGQKKWLNKSECRNINRTYCDLSAETSDYEHQYYAKVKAIWGTKCSKWAES 126

Qy     149 PRFTPWWETKIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYY-ELLYRVFII 207
           || |: ||:| || : :|    |: |:| ||    |  ::  ||::  |  | | | ::
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Db     127 GRFYPFLETQIGPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQQIYSNLKYNVSVL 186

Qy     208 NNSLEKEQKVYEGAHRAVEIEALTPHSSYCVVAEIYQPMLDRRSQRSEERC 258
           |    :        |  | :  | |:: |||  | : |   ||:| ||::|
Db     187 NTKSNRTWSQCVTNHTLV-LTWLEPNTLYCVHVESFVPGPPRRAQPSEKQC 236


RESULT 9
US-08-943-087-22
; Sequence 22, Application US/08943087
; Patent No. 5945511
;  GENERAL INFORMATION:
;    APPLICANT:  Lok, Si
;    APPLICANT:  Kho, Choon J.
;    APPLICANT:  Jelmberg, Anna C.
;    APPLICANT:  Adams, Robyn L.
;    APPLICANT:  Whitmore, Theodore E.
;    APPLICANT:  Farrah, Theresa M.
;    TITLE OF INVENTION:  CYTOKINE RECEPTOR
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ZymoGenetics, Inc.
;      STREET:  1201 Eastlake Avenue East
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98102
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/943,087
;      FILING DATE:
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/803,305
;      FILING DATE:  20-FEB-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lunn, Paul G
;      REGISTRATION NUMBER:  32,743
;      REFERENCE/DOCKET NUMBER:  96-24C1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206-442-6627
;      TELEFAX:  206-442-6678
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  22:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  553 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FRAGMENT TYPE:  internal
US-08-943-087-22

  Query Match             21.7%;  Score 310;  DB 2;  Length 553;
  Best Local Similarity   32.0%;  Pred. No. 7.2e-27;
  Matches   74;  Conservative   33;  Mismatches   90;  Indels   34;  Gaps    3;

Qy      29 KPQRVQFQSRNFHNILQWQPGRALTGNSSVYFVQYKIMFSCSMKSSHQKPSGCWQHISCN 88
           ||  : | | |  |:||| |   | |    | ||| |
Db      39 KPANITFLSINMKNVLQWTPPEGLQGVKVTYTVQYFI---------------------- 75

Qy      89 FPGCRTLAKYGQRQWKNKEDCWGTQELSCDLTSETSDIQEPYYGRVRAASAGSYSEWSMT 148
                 |||::| || :|       |||::|||| :  || :|:|      |:|: :
Db      76 ---------YGQKKWLNKSECRNINRTYCDLSAETSDYEHQYYAKVKAIWGTKCSKWAES 126

Qy     149 PRFTPWWETKIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYY-ELLYRVFII 207
           || |: ||:| || : :|    |: |:| ||    |  ::  ||::  |  | | | ::
Db     127 GRFYPFLETQIGPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQQIYSNLKYNVSVL 186
```

```
Qy     208 NNSLEKEQKVYEGAHRAVEIEALTPHSSYCVVAEIYQPMLDRRSQRSEERC 258
           |    :        |  | :  | |:: |||  | : |   ||:| ||::|
Db     187 NTKSNRTWSQCVTNHTLV-LTWLEPNTLYCVHVESFVPGPPRRAQPSEKQC 236
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RESULT 10
US-08-943-087-24
; Sequence 24, Application US/08943087
; Patent No. 5945511
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Farrah, Theresa M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,087
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/803,305
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-24C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-943-087-24

Query Match 21.7%; Score 310; DB 2; Length 553;
Best Local Similarity 32.0%; Pred. No. 7.2e-27;
Matches 74; Conservative 33; Mismatches 90; Indels 34; Gaps 3;

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Qy      29 KPQRVQFQSRNFHNILQWQPGRALTGNSSVYFVQYKIMFSCSMKSSHQKPSGCWQHISCN 88
           ||  : | | |  |:||| |   | |    | ||| |
Db      39 KPANITFLSINMKNVLQWTPPEGLQGVKVTYTVQYFI---------------------- 75

Qy      89 FPGCRTLAKYGQRQWKNKEDCWGTQELSCDLTSETSDIQEPYYGRVRAASAGSYSEWSMT 148
                  |||::| || :|       |||::|||| :  || :|:|      |:|: :
Db      76 ---------YGQKKWLNKSECRNINRTYCDLSAETSDYEHQYYAKVKAIWGTKCSKWAES 126

Qy     149 PRFTPWWETKIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYY-ELLYRVFII 207
            || |: ||:| || : :|    |: |:| ||    |  ::  ||::  |  | | | ::
Db     127 GRFYPFLETQIGPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQQIYSNLKYNVSVL 186

Qy     208 NNSLEKEQKVYEGAHRAVEIEALTPHSSYCVVAEIYQPMLDRRSQRSEERC 258
           |    :        |  | :  | |:: |||  | : |   ||:| ||::|
```

```
Db     187 NTKSNRTWSQCVTNHTLV-LTWLEPNTLYCVHVESFVPGPPRRAQPSEKQC 236
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RESULT 11
US-08-943-087-26
; Sequence 26, Application US/08943087
; Patent No. 5945511
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Farrah, Theresa M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,087
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/803,305
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-24C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-943-087-26

Query Match 21.7%; Score 310; DB 2; Length 553;
Best Local Similarity 32.0%; Pred. No. 7.2e-27;
Matches 74; Conservative 33; Mismatches 90; Indels 34; Gaps 3;

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RESULT 12
US-08-943-087-28
; Sequence 28, Application US/08943087
; Patent No. 5945511
;  GENERAL INFORMATION:
;    APPLICANT:  Lok, Si
;    APPLICANT:  Kho, Choon J.
;    APPLICANT:  Jelmberg, Anna C.
;    APPLICANT:  Adams, Robyn L.
;    APPLICANT:  Whitmore, Theodore E.
;    APPLICANT:  Farrah, Theresa M.
;    TITLE OF INVENTION:  CYTOKINE RECEPTOR
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ZymoGenetics, Inc.
;      STREET:  1201 Eastlake Avenue East
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98102
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/943,087
;      FILING DATE:
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/803,305
;      FILING DATE:  20-FEB-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lunn, Paul G
;      REGISTRATION NUMBER:  32,743
;      REFERENCE/DOCKET NUMBER:  96-24C1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206-442-6627
;      TELEFAX:  206-442-6678
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  28:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  553 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FRAGMENT TYPE:  internal
US-08-943-087-28

  Query Match             21.7%;  Score 310;  DB 2;  Length 553;
  Best Local Similarity   32.0%;  Pred. No. 7.2e-27;
  Matches   74;  Conservative   33;  Mismatches   90;  Indels   34;  Gaps    3;

Qy      29 KPQRVQFQSRNFHNILQWQPGRALTGNSSVYFVQYKIMFSCSMKSSHQKPSGCWQHISCN 88
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Db      39 KPANITFLSINMKNVLQWTPPEGLQGVKVTYTVQYFI---------------------- 75

Qy      89 FPGCRTLAKYGQRQWKNKEDCWGTQELSCDLTSETSDIQEPYYGRVRAASAGSYSEWSMT 148
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Qy     149 PRFTPWWETKIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYY-ELLYRVFII 207
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Db     127 GRFYPFLETQIGPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQQIYSNLKYNVSVL 186

Qy     208 NNSLEKEQKVYEGAHRAVEIEALTPHSSYCVVAEIYQPMLDRRSQRSEERC 258
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Db     187 NTKSNRTWSQCVTNHTLV-LTWLEPNTLYCVHVESFVPGPPRRAQPSEKQC 236


RESULT 13
US-08-943-087-30
; Sequence 30, Application US/08943087
; Patent No. 5945511
;  GENERAL INFORMATION:
;    APPLICANT:  Lok, Si
;    APPLICANT:  Kho, Choon J.
;    APPLICANT:  Jelmberg, Anna C.
;    APPLICANT:  Adams, Robyn L.
;    APPLICANT:  Whitmore, Theodore E.
;    APPLICANT:  Farrah, Theresa M.
;    TITLE OF INVENTION:  CYTOKINE RECEPTOR
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ZymoGenetics, Inc.
;      STREET:  1201 Eastlake Avenue East
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98102
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/943,087
;      FILING DATE:
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/803,305
;      FILING DATE:  20-FEB-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lunn, Paul G
;      REGISTRATION NUMBER:  32,743
;      REFERENCE/DOCKET NUMBER:  96-24C1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206-442-6627
;      TELEFAX:  206-442-6678
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  30:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  553 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FRAGMENT TYPE:  internal
US-08-943-087-30

  Query Match             21.7%;  Score 310;  DB 2;  Length 553;
  Best Local Similarity   32.0%;  Pred. No. 7.2e-27;
  Matches   74;  Conservative   33;  Mismatches   90;  Indels   34;  Gaps    3;

Qy      29 KPQRVQFQSRNFHNILQWQPGRALTGNSSVYFVQYKIMFSCSMKSSHQKPSGCWQHISCN 88
           ||  : | | |  |:||| |   | |    | ||| |
Db      39 KPANITFLSINMKNVLQWTPPEGLQGVKVTYTVQYFI---------------------- 75

Qy      89 FPGCRTLAKYGQRQWKNKEDCWGTQELSCDLTSETSDIQEPYYGRVRAASAGSYSEWSMT 148
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Qy     149 PRFTPWWETKIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYY-ELLYRVFII 207
            || |: ||:| || : :|    |: |:| ||    |  ::  ||::  |  | | | ::
Db     127 GRFYPFLETQIGPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQQIYSNLKYNVSVL 186

Qy     208 NNSLEKEQKVYEGAHRAVEIEALTPHSSYCVVAEIYQPMLDRRSQRSEERC 258
           |    :        |  | :  | |:: |||  | : |   ||:| ||::|
Db     187 NTKSNRTWSQCVTNHTLV-LTWLEPNTLYCVHVESFVPGPPRRAQPSEKQC 236


RESULT 14
US-08-943-087-32
; Sequence 32, Application US/08943087
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; Patent No. 5945511
;  GENERAL INFORMATION:
;    APPLICANT:  Lok, Si
;    APPLICANT:  Kho, Choon J.
;    APPLICANT:  Jelmberg, Anna C.
;    APPLICANT:  Adams, Robyn L.
;    APPLICANT:  Whitmore, Theodore E.
;    APPLICANT:  Farrah, Theresa M.
;    TITLE OF INVENTION:  CYTOKINE RECEPTOR
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ZymoGenetics, Inc.
;      STREET:  1201 Eastlake Avenue East
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98102
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/943,087
;      FILING DATE:
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/803,305
;      FILING DATE:  20-FEB-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lunn, Paul G
;      REGISTRATION NUMBER:  32,743
;      REFERENCE/DOCKET NUMBER:  96-24C1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206-442-6627
;      TELEFAX:  206-442-6678
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  32:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  553 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FRAGMENT TYPE:  internal
US-08-943-087-32

  Query Match             21.7%;  Score 310;  DB 2;  Length 553;
  Best Local Similarity   32.0%;  Pred. No. 7.2e-27;
  Matches   74;  Conservative   33;  Mismatches   90;  Indels   34;  Gaps    3;

Qy      29 KPQRVQFQSRNFHNILQWQPGRALTGNSSVYFVQYKIMFSCSMKSSHQKPSGCWQHISCN 88
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Qy      89 FPGCRTLAKYGQRQWKNKEDCWGTQELSCDLTSETSDIQEPYYGRVRAASAGSYSEWSMT 148
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; Sequence 34, Application US/08943087
; Patent No. 5945511
;  GENERAL INFORMATION:
;    APPLICANT:  Lok, Si
;    APPLICANT:  Kho, Choon J.
;    APPLICANT:  Jelmberg, Anna C.
;    APPLICANT:  Adams, Robyn L.
;    APPLICANT:  Whitmore, Theodore E.
;    APPLICANT:  Farrah, Theresa M.
;    TITLE OF INVENTION:  CYTOKINE RECEPTOR
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ZymoGenetics, Inc.
;      STREET:  1201 Eastlake Avenue East
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98102
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/943,087
;      FILING DATE:
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/803,305
;      FILING DATE:  20-FEB-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lunn, Paul G
;      REGISTRATION NUMBER:  32,743
;      REFERENCE/DOCKET NUMBER:  96-24C1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206-442-6627
;      TELEFAX:  206-442-6678
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  34:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  553 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FRAGMENT TYPE:  internal
US-08-943-087-34

  Query Match             21.7%;  Score 310;  DB 2;  Length 553;
  Best Local Similarity   32.0%;  Pred. No. 7.2e-27;
  Matches   74;  Conservative   33;  Mismatches   90;  Indels   34;  Gaps    3;

Qy      29 KPQRVQFQSRNFHNILQWQPGRALTGNSSVYFVQYKIMFSCSMKSSHQKPSGCWQHISCN 88
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Qy      89 FPGCRTLAKYGQRQWKNKEDCWGTQELSCDLTSETSDIQEPYYGRVRAASAGSYSEWSMT 148
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Qy     149 PRFTPWWETKIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYY-ELLYRVFII 207
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Qy     208 NNSLEKEQKVYEGAHRAVEIEALTPHSSYCVVAEIYQPMLDRRSQRSEERC 258
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Job time : 28 secs
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GenCore version 5.1.3

OM protein - protein search, using sw model

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(without alignments)
219.602 Million cell updates/sec

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Perfect score: 1427
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 106657 seqs, 16763532 residues

Total number of hits satisfying chosen parameters: 106657

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1213	85.0	231	10	US-09-728-911-2	Sequence 2, Appli
2	1213	85.0	231	10	US-09-949-192-6	Sequence 6, Appli
3	1104	77.4	210	10	US-09-728-911-13	Sequence 13, Appl
4	310	21.7	207	10	US-09-746-359A-65	Sequence 65, Appl
5	310	21.7	214	10	US-09-746-359A-63	Sequence 63, Appl
6	310	21.7	217	10	US-09-746-359A-55	Sequence 55, Appl
7	310	21.7	221	10	US-09-746-359A-12	Sequence 12, Appl
8	310	21.7	542	12	US-10-052-586-398	Sequence 398, App
9	310	21.7	547	10	US-09-746-359A-54	Sequence 54, Appl
10	310	21.7	553	10	US-09-746-359A-11	Sequence 11, Appl
11	310	21.7	553	10	US-09-949-192-7	Sequence 7, Appli
12	310	21.7	559	10	US-09-746-359A-62	Sequence 62, Appl
13	310	21.7	571	10	US-09-746-359A-53	Sequence 53, Appl
14	310	21.7	594	10	US-09-746-359A-23	Sequence 23, Appl
15	289	20.3	56	10	US-09-864-761-40289	Sequence 40289, A
16	289	20.3	56	10	US-09-864-761-47623	Sequence 47623, A
17	276	19.3	217	10	US-09-746-359A-38	Sequence 38, Appl
18	276	19.3	514	10	US-09-746-359A-39	Sequence 39, Appl
19	276	19.3	546	10	US-09-746-359A-37	Sequence 37, Appl
20	240	16.8	574	9	US-09-912-672A-2	Sequence 2, Appli
21	240	16.8	574	9	US-10-063-547-164	Sequence 164, App
22	240	16.8	574	10	US-09-728-911-25	Sequence 25, Appl
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24	240	16.8	574	12	US-10-006-867-164	Sequence 164, App
25	237	16.6	211	10	US-09-728-911-34	Sequence 34, Appl
26	237	16.6	212	9	US-09-912-672A-6	Sequence 6, Appli
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28	211	14.8	150	10	US-09-746-359A-66	Sequence 66, Appl
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33	155.5	10.9	219	10	US-09-355-000-7	Sequence 7, Appli
34	153.5	10.8	219	10	US-09-355-000-8	Sequence 8, Appli
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36	152.5	10.7	578	9	US-09-912-672A-27	Sequence 27, Appl
37	152	10.7	211	10	US-09-728-911-36	Sequence 36, Appl
38	151.5	10.6	196	10	US-09-746-359A-67	Sequence 67, Appl
39	151.5	10.6	201	9	US-09-912-672A-16	Sequence 16, Appl
40	151.5	10.6	201	10	US-09-746-359A-59	Sequence 59, Appl
41	151.5	10.6	203	10	US-09-746-359A-15	Sequence 15, Appl
42	151.5	10.6	282	9	US-09-912-672A-15	Sequence 15, Appl
43	151.5	10.6	307	10	US-09-746-359A-58	Sequence 58, Appl
44	151.5	10.6	311	9	US-09-978-295A-352	Sequence 352, App
45	151.5	10.6	311	9	US-09-992-598-183	Sequence 183, App

ALIGNMENTS

RESULT 1
US-09-728-911-2
; Sequence 2, Application US/09728911
; Patent No. US20020012669A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Kindsvogel, Wayne
; APPLICANT: Chen, Zhi
; TITLE OF INVENTION: Human Cytokine Receptor
; FILE REFERENCE: 99-93
; CURRENT APPLICATION NUMBER: US/09/728,911
; CURRENT FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 60/169,049
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: US 60/232,219
; PRIOR FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: US 60/244,610
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-728-911-2

Query Match 85.0%; Score 1213; DB 10; Length 231;
Best Local Similarity 87.8%; Pred. No. 2.4e-109;
Matches 230; Conservative 0; Mismatches 0; Indels 32; Gaps 1;

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RESULT 2
US-09-949-192-6
; Sequence 6, Application US/09949192
; Patent No. US20020142292A1
; GENERAL INFORMATION:
;  APPLICANT: Parham, Christi L.
;  APPLICANT:  Gorman, Daniel L.
;  APPLICANT:  Kurata, Hirokazu
;  APPLICANT:  Arai, Naoko
;  APPLICANT:  Sana, Theodore R.
;  APPLICANT:  Mattson, Jeanine D.
;  APPLICANT:  Murphy, Erin E.
;  APPLICANT:  Savkoor, Chetan
;  APPLICANT:  Grein, Jeffery
;  APPLICANT:  Smith, Kathleen M.
;  APPLICANT:  McClanahan, Terrill K.
;  TITLE OF INVENTION: MAMMALIAN GENES; RELATED REAGENTS AND METHODS
;  FILE REFERENCE: DX01169K
;  CURRENT APPLICATION NUMBER: US/09/949,192
;  CURRENT FILING DATE:  2001-09-07
;  PRIOR APPLICATION NUMBER: 60/231,267
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 53
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
;   LENGTH: 231
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-949-192-6

  Query Match             85.0%;  Score 1213;  DB 10;  Length 231;
  Best Local Similarity   87.8%;  Pred. No. 2.4e-109;
  Matches  230;  Conservative    0;  Mismatches    0;  Indels   32;  Gaps    1;

Qy       1 MPKHCFLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVYF 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2 MPKHCFLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVYF 61

Qy      61 VQYKIMFSCSMKSSHQKPSGCWQHISCNFPGCRTLAKYGQRQWKNKEDCWGTQELSCDLT 120
           |||||                                |||||||||||||||||||||||
Db      62 VQYKI--------------------------------YGQRQWKNKEDCWGTQELSCDLT 89

Qy     121 SETSDIQEPYYGRVRAASAGSYSEWSMTPRFTPWWETKIDPPVMNITQVNGSLLVILHAP 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      90 SETSDIQEPYYGRVRAASAGSYSEWSMTPRFTPWWETKIDPPVMNITQVNGSLLVILHAP 149

Qy     181 NLPYRYQKEKNVSIEDYYELLYRVFIINNSLEKEQKVYEGAHRAVEIEALTPHSSYCVVA 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     150 NLPYRYQKEKNVSIEDYYELLYRVFIINNSLEKEQKVYEGAHRAVEIEALTPHSSYCVVA 209

Qy     241 EIYQPMLDRRSQRSEERCVEIP 262
           |||||||||||||||||||||||
Db     210 EIYQPMLDRRSQRSEERCVEIP 231


RESULT 3
US-09-728-911-13
; Sequence 13, Application US/09728911
; Patent No. US20020012669A1
; GENERAL INFORMATION:
;  APPLICANT:  Presnell, Scott R.
;  APPLICANT:  Xu, Wenfeng
;  APPLICANT:  Kindsvogel, Wayne
;  APPLICANT:  Chen, Zhi
;  TITLE OF INVENTION:  Human Cytokine Receptor
;  FILE REFERENCE:  99-93
;  CURRENT APPLICATION NUMBER: US/09/728,911
;  CURRENT FILING DATE:  2000-12-01
;  PRIOR APPLICATION NUMBER:  US 60/169,049
;  PRIOR FILING DATE:  1999-12-03
;  PRIOR APPLICATION NUMBER:  US 60/232,219
;  PRIOR FILING DATE:  2000-09-13
;  PRIOR APPLICATION NUMBER:  US 60/244,610
;  PRIOR FILING DATE:  2000-10-31
;  NUMBER OF SEQ ID NOS:  36
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 13
;   LENGTH: 210
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-728-911-13

  Query Match             77.4%;  Score 1104;  DB 10;  Length 210;
  Best Local Similarity   86.8%;  Pred. No. 6.3e-99;
  Matches  210;  Conservative    0;  Mismatches    0;  Indels   32;  Gaps    1;

Qy      21 TQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVYFVQYKIMFSCSMKSSHQKPSG 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 TQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVYFVQYKI---------------- 45

Qy      81 CWQHISCNFPGCRTLAKYGQRQWKNKEDCWGTQELSCDLTSETSDIQEPYYGRVRAASAG 140
                           ||||||||||||||||||||||||||||||||||||||||||||
Db      46 -----------------YGQRQWKNKEDCWGTQELSCDLTSETSDIQEPYYGRVRAASAG 88

Qy     141 SYSEWSMTPRFTPWWETKIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYYEL 200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      89 SYSEWSMTPRFTPWWETKIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYYEL 148

Qy     201 LYRVFIINNSLEKEQKVYEGAHRAVEIEALTPHSSYCVVAEIYQPMLDRRSQRSEERCVE 260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     149 LYRVFIINNSLEKEQKVYEGAHRAVEIEALTPHSSYCVVAEIYQPMLDRRSQRSEERCVE 208

Qy     261 IP 262
           ||
Db     209 IP 210


RESULT 4
US-09-746-359A-65
; Sequence 65, Application US/09746359A
; Patent No. US20020042366A1
; GENERAL INFORMATION:
;  APPLICANT: Thompson, Penny
;  APPLICANT:  Foster, Donald C.
;  APPLICANT:  Xu, Wenfeng
;  APPLICANT:  Madden, Karen L.
;  APPLICANT:  Kelly, James D.
;  APPLICANT:  Sprecher, Cindy A.
;  APPLICANT:  Blumberg, Hal
;  APPLICANT:  Eagan, Maribeth A.
;  APPLICANT:  Jaspers, Stephen R.
;  APPLICANT:  Chandrasekher, Yasmin A.
;  APPLICANT:  No. US20020042366A1ak, Julia E.
;  TITLE OF INVENTION: Method for Treating Inflammation
;  FILE REFERENCE: 99-108
;  CURRENT APPLICATION NUMBER: US/09/746,359A
;  CURRENT FILING DATE:  2001-05-21
;  PRIOR APPLICATION NUMBER: 60/171,969
;  PRIOR FILING DATE: 1999-12-23
;  PRIOR APPLICATION NUMBER: 60/213,341
;  PRIOR FILING DATE: 2000-06-22
;  NUMBER OF SEQ ID NOS: 72
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 65
;   LENGTH: 207
;   TYPE: PRT
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;   ORGANISM: Homo sapiens
US-09-746-359A-65

  Query Match             21.7%;  Score 310;  DB 10;  Length 207;
  Best Local Similarity   32.0%;  Pred. No. 1.3e-22;
  Matches   74;  Conservative   33;  Mismatches   90;  Indels   34;  Gaps    3;

Qy      29 KPQRVQFQSRNFHNILQWQPGRALTGNSSVYFVQYKIMFSCSMKSSHQKPSGCWQHISCN 88
           ||  : | | |  |:||| |   | |    | ||| |
Db       3 KPANITFLSINMKNVLQWTPPEGLQGVKVTYTVQYFI---------------------- 39

Qy      89 FPGCRTLAKYGQRQWKNKEDCWGTQELSCDLTSETSDIQEPYYGRVRAASAGSYSEWSMT 148
                 |||:: | || :|       |||::|||| :  || :|:|      |:|: :
Db      40 ---------YGQKKWLNKSECRNINRTYCDLSAETSDYEHQYYAKVKAIWGTKCSKWAES 90

Qy     149 PRFTPWWETKIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYY-ELLYRVFII 207
            || |: ||:| || : :|    |: |:| ||    |  ::  ||::  |  | | | ::
Db      91 GRFYPFLETQIGPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQQIYSNLKYNVSVL 150

        208 NNSLEKEQKVYEGAHRAVEIEALTPHSSYCVVAEIYQPMLDRRSQRSEERC 258
            |    :       |  | :  | |:: |||  |.: |   ||:| ||::|
        151 NTKSNRTWSQCVTNHTLV-LTWLEPNTLYCVHVESFVPGPPRRAQPSEKQC 200


RESULT 5
US-09-746-359A-63
; Sequence 63, Application US/09746359A
; Patent No. US20020042366A1
; GENERAL INFORMATION:
;  APPLICANT: Thompson, Penny
;  APPLICANT:  Foster, Donald C.
;  APPLICANT:  Xu, Wenfeng
;  APPLICANT:  Madden, Karen L.
;  APPLICANT:  Kelly, James D.
;  APPLICANT:  Sprecher, Cindy A.
;  APPLICANT:  Blumberg, Hal
;  APPLICANT:  Eagan, Maribeth A.
;  APPLICANT:  Jaspers, Stephen R.
;  APPLICANT:  Chandrasekher, Yasmin A.
;  APPLICANT:  No. US20020042366A1ak, Julia E.
;  TITLE OF INVENTION: Method for Treating Inflammation
;  FILE REFERENCE: 99-108
;  CURRENT APPLICATION NUMBER: US/09/746,359A
;  CURRENT FILING DATE:  2001-05-21
;  PRIOR APPLICATION NUMBER: 60/171,969
;  PRIOR FILING DATE: 1999-12-23
;  PRIOR APPLICATION NUMBER: 60/213,341
;  PRIOR FILING DATE: 2000-06-22
;  NUMBER OF SEQ ID NOS: 72
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 63
;   LENGTH: 214
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-746-359A-63

  Query Match             21.7%;  Score 310;  DB 10;  Length 214;
  Best Local Similarity   32.0%;  Pred. No. 1.3e-22;
  Matches   74;  Conservative   33;  Mismatches   90;  Indels   34;  Gaps    3;

Qy      29 KPQRVQFQSRNFHNILQWQPGRALTGNSSVYFVQYKIMFSCSMKSSHQKPSGCWQHISCN 88
           ||  : | | |  |:||| |   | |    | ||| |
Db      10 KPANITFLSINMKNVLQWTPPEGLQGVKVTYTVQYFI---------------------- 46

Qy      89 FPGCRTLAKYGQRQWKNKEDCWGTQELSCDLTSETSDIQEPYYGRVRAASAGSYSEWSMT 148
                 |||:: | || :|       |||::|||| :  || :|:|      |:|: :
Db      47 ---------YGQKKWLNKSECRNINRTYCDLSAETSDYEHQYYAKVKAIWGTKCSKWAES 97

Qy     149 PRFTPWWETKIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYY-ELLYRVFII 207
            || |: ||:| || : :|    |: |:| ||    |  ::  ||::  |  | | | ::
Db      98 GRFYPFLETQIGPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQQIYSNLKYNVSVL 157

Qy     208 NNSLEKEQKVYEGAHRAVEIEALTPHSSYCVVAEIYQPMLDRRSQRSEERC 258
            |    :       |  | :  | |:: |||  |.: |   ||:| ||::|
Db     158 NTKSNRTWSQCVTNHTLV-LTWLEPNTLYCVHVESFVPGPPRRAQPSEKQC 207


RESULT 6
US-09-746-359A-55
; Sequence 55, Application US/09746359A
; Patent No. US20020042366A1
; GENERAL INFORMATION:
;  APPLICANT: Thompson, Penny
;  APPLICANT:  Foster, Donald C.
;  APPLICANT:  Xu, Wenfeng
;  APPLICANT:  Madden, Karen L.
;  APPLICANT:  Kelly, James D.
;  APPLICANT:  Sprecher, Cindy A.
;  APPLICANT:  Blumberg, Hal
;  APPLICANT:  Eagan, Maribeth A.
;  APPLICANT:  Jaspers, Stephen R.
;  APPLICANT:  Chandrasekher, Yasmin A.
;  APPLICANT:  No. US20020042366A1ak, Julia E.
;  TITLE OF INVENTION: Method for Treating Inflammation
;  FILE REFERENCE: 99-108
;  CURRENT APPLICATION NUMBER: US/09/746,359A
;  CURRENT FILING DATE:  2001-05-21
;  PRIOR APPLICATION NUMBER: 60/171,969
;  PRIOR FILING DATE: 1999-12-23
;  PRIOR APPLICATION NUMBER: 60/213,341
;  PRIOR FILING DATE: 2000-06-22
;  NUMBER OF SEQ ID NOS: 72
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 55
;   LENGTH: 217
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-746-359A-55

  Query Match             21.7%;  Score 310;  DB 10;  Length 217;
  Best Local Similarity   32.0%;  Pred. No. 1.4e-22;
  Matches   74;  Conservative   33;  Mismatches   90;  Indels   34;  Gaps    3;

Qy      29 KPQRVQFQSRNFHNILQWQPGRALTGNSSVYFVQYKIMFSCSMKSSHQKPSGCWQHISCN 88
           ||  : | | |  |:||| |   | |    | ||| |
Db      10 KPANITFLSINMKNVLQWTPPEGLQGVKVTYTVQYFI---------------------- 46

Qy      89 FPGCRTLAKYGQRQWKNKEDCWGTQELSCDLTSETSDIQEPYYGRVRAASAGSYSEWSMT 148
                 |||:: | || :|       |||::|||| :  || :|:|      |:|: :
Db      47 ---------YGQKKWLNKSECRNINRTYCDLSAETSDYEHQYYAKVKAIWGTKCSKWAES 97

Qy     149 PRFTPWWETKIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYY-ELLYRVFII 207
            || |: ||:| || : :|    |: |:| ||    |  ::  ||::  |  | | | ::
Db      98 GRFYPFLETQIGPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQQIYSNLKYNVSVL 157

Qy     208 NNSLEKEQKVYEGAHRAVEIEALTPHSSYCVVAEIYQPMLDRRSQRSEERC 258
            |    :       |  | :  | |:: |||  |.: |   ||:| ||::|
Db     158 NTKSNRTWSQCVTNHTLV-LTWLEPNTLYCVHVESFVPGPPRRAQPSEKQC 207


RESULT 7
US-09-746-359A-12
; Sequence 12, Application US/09746359A
; Patent No. US20020042366A1
; GENERAL INFORMATION:
;  APPLICANT: Thompson, Penny
;  APPLICANT:  Foster, Donald C.
;  APPLICANT:  Xu, Wenfeng
;  APPLICANT:  Madden, Karen L.
;  APPLICANT:  Kelly, James D.
;  APPLICANT:  Sprecher, Cindy A.
;  APPLICANT:  Blumberg, Hal
;  APPLICANT:  Eagan, Maribeth A.
;  APPLICANT:  Jaspers, Stephen R.
;  APPLICANT:  Chandrasekher, Yasmin A.
;  APPLICANT:  No. US20020042366A1ak, Julia E.
```

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;  TITLE OF INVENTION: Method for Treating Inflammation
;  FILE REFERENCE: 99-108
;  CURRENT APPLICATION NUMBER: US/09/746,359A
;  CURRENT FILING DATE:  2001-05-21
;  PRIOR APPLICATION NUMBER: 60/171,969
;  PRIOR FILING DATE: 1999-12-23
;  PRIOR APPLICATION NUMBER: 60/213,341
;  PRIOR FILING DATE: 2000-06-22
;  NUMBER OF SEQ ID NOS: 72
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 12
;   LENGTH: 221
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-746-359A-12

  Query Match             21.7%;  Score 310;  DB 10;  Length 221;
  Best Local Similarity   32.0%;  Pred. No. 1.4e-22;
  Matches   74;  Conservative   33;  Mismatches   90;  Indels   34;  Gaps    3;

Qy      29 KPQRVQFQSRNFHNILQWQPGRALTGNSSVYFVQYKIMFSCSMKSSHQKPSGCWQHISCN 88
           ||  : | | |  |:||| |   | |    | ||| |
Db      10 KPANITFLSINMKNVLQWTPPEGLQGVKVTYTVQYFI---------------------- 46

Qy      89 FPGCRTLAKYGQRQWKNKEDCWGTQELSCDLTSETSDIQEPYYGRVRAASAGSYSEWSMT 148
                 |||::| || :|       |||::|||| :  || :|:|      |:|: :
Db      47 ---------YGQKKWLNKSECRNINRTYCDLSAETSDYEHQYYAKVKAIWGTKCSKWAES 97

Qy     149 PRFTPWWETKIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYY-ELLYRVFII 207
           || |: ||:| || : :|    |: |:| ||    |  ::  ||::  |  | | | ::
Db      98 GRFYPFLETQIGPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQQIYSNLKYNVSVL 157

Qy     208 NNSLEKEQKVYEGAHRAVEIEALTPHSSYCVVAEIYQPMLDRRSQRSEERC 258
           |    :       | | :  | |:: |||  | : |   ||:| ||::|
Db     158 NTKSNRTWSQCVTNHTLV-LTWLEPNTLYCVHVESFVPGPPRRAQPSEKQC 207


RESULT 8
US-10-052-586-398
; Sequence 398, Application US/10052586
; Patent No. US20020127584A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Chen,Jian
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Pan,James
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  APPLICANT:  Zhang,Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3430R1C1
;  CURRENT APPLICATION NUMBER: US/10/052,586
;  CURRENT FILING DATE:  2002-01-15
;  PRIOR APPLICATION NUMBER: 60/059263
;  PRIOR FILING DATE: 1997-09-18
;  PRIOR APPLICATION NUMBER: 60/059266
;  PRIOR FILING DATE: 1997-09-18
;  PRIOR APPLICATION NUMBER: 60/062250
;  PRIOR FILING DATE: 1997-10-17
;  PRIOR APPLICATION NUMBER: 60/063120
;  PRIOR FILING DATE: 1997-10-24
;  PRIOR APPLICATION NUMBER: 60/063121
;  PRIOR FILING DATE: 1997-10-24
;  PRIOR APPLICATION NUMBER: 60/063486
;  PRIOR FILING DATE: 1997-10-21
;  PRIOR APPLICATION NUMBER: 60/063540
;  PRIOR FILING DATE: 1997-10-28
;  PRIOR APPLICATION NUMBER: 60/063541
;  PRIOR FILING DATE: 1997-10-28
;  PRIOR APPLICATION NUMBER: 60/063544
;  PRIOR FILING DATE: 1997-10-28
;  PRIOR APPLICATION NUMBER: 60/063564
;  PRIOR FILING DATE: 1997-10-28
;  PRIOR APPLICATION NUMBER: 60/063734
;  PRIOR FILING DATE: 1997-10-29
;  PRIOR APPLICATION NUMBER: 60/063870
;  PRIOR FILING DATE: 1997-10-31
;  PRIOR APPLICATION NUMBER: 60/064103
;  PRIOR FILING DATE: 1997-10-31
;  PRIOR APPLICATION NUMBER: 60/065311
;  PRIOR FILING DATE: 1997-11-13
;  PRIOR APPLICATION NUMBER: 60/066120
;  PRIOR FILING DATE: 1997-11-21
;  PRIOR APPLICATION NUMBER: 60/066466
;  PRIOR FILING DATE: 1997-11-24
;  PRIOR APPLICATION NUMBER: 60/066772
;  PRIOR FILING DATE: 1997-11-24
;  PRIOR APPLICATION NUMBER: 60/069335
;  PRIOR FILING DATE: 1997-12-11
;  PRIOR APPLICATION NUMBER: 60/069425
;  PRIOR FILING DATE: 1997-12-12
;  PRIOR APPLICATION NUMBER: 60/069870
;  PRIOR FILING DATE: 1997-12-17
;  PRIOR APPLICATION NUMBER: 60/068017
;  PRIOR FILING DATE: 1997-12-18
;  PRIOR APPLICATION NUMBER: 60/077450
;  PRIOR FILING DATE: 1998-03-10
;  PRIOR APPLICATION NUMBER: 60/077632
;  PRIOR FILING DATE: 1998-03-11
;  PRIOR APPLICATION NUMBER: 60/077649
;  PRIOR FILING DATE: 1998-03-11
;  PRIOR APPLICATION NUMBER: 60/078886
;  PRIOR FILING DATE: 1998-03-20
;  PRIOR APPLICATION NUMBER: 60/078939
;  PRIOR FILING DATE: 1998-03-20
;  PRIOR APPLICATION NUMBER: 60/079664
;  PRIOR FILING DATE: 1998-03-27
;  PRIOR APPLICATION NUMBER: 60/079786
;  PRIOR FILING DATE: 1998-03-27
;  PRIOR APPLICATION NUMBER: 60/080107
;  PRIOR FILING DATE: 1998-03-31
;  PRIOR APPLICATION NUMBER: 60/080194
;  PRIOR FILING DATE: 1998-03-31
;  PRIOR APPLICATION NUMBER: 60/080327
;  PRIOR FILING DATE: 1998-04-01
;  PRIOR APPLICATION NUMBER: 60/080333
;  PRIOR FILING DATE: 1998-04-01
;  PRIOR APPLICATION NUMBER: 60/081049
;  PRIOR FILING DATE: 1998-04-08
;  PRIOR APPLICATION NUMBER: 60/081070
;  PRIOR FILING DATE: 1998-04-08
;  PRIOR APPLICATION NUMBER: 60/081195
;  PRIOR FILING DATE: 1998-04-09
;  PRIOR APPLICATION NUMBER: 60/081838
;  PRIOR FILING DATE: 1998-04-15
;  PRIOR APPLICATION NUMBER: 60/082568
;  PRIOR FILING DATE: 1998-04-21
;  PRIOR APPLICATION NUMBER: 60/082569
;  PRIOR FILING DATE: 1998-04-21
;  PRIOR APPLICATION NUMBER: 60/082704
;  PRIOR FILING DATE: 1998-04-22
;  PRIOR APPLICATION NUMBER: 60/082797
;  PRIOR FILING DATE: 1998-04-22
;  PRIOR APPLICATION NUMBER: 60/083322
;  PRIOR FILING DATE: 1998-04-28
;  PRIOR APPLICATION NUMBER: 60/083495
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/083496
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/083499
;  PRIOR FILING DATE: 1998-04-29
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; PRIOR APPLICATION NUMBER: 60/083559
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/084366
; PRIOR FILING DATE: 1998-05-05
; PRIOR APPLICATION NUMBER: 60/084414
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084639
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084640
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084643
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085582
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/086023
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/086392
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/086486
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087098
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087208
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087609
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087827
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: 60/088025
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088028
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088029
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088033
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088167
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088202
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088212
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088217
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088326
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088655
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: 60/088722
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088738
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088740
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088811
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088824
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088825
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088826
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088861
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/088863
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/088876
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/089090
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: 60/089105
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: 60/089512
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089514
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089538
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089598
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089653
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089908

Query Match 21.7%; Score 310; DB 12; Length 542;
Best Local Similarity 32.0%; Pred. No. 4.6e-22;
Matches 74; Conservative 33; Mismatches 90; Indels 34; Gaps 3;

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Qy      29 KPQRVQFQSRNFHNILQWQPGRALTGNSSVYFVQYKIMFSCSMKSSHQKPSGCWQHISCN 88
           ||  : | | |  |:||| |   | |    | ||| |
Db      28 KPANITFLSINMKNVLQWTPPEGLQGVKVTYTVQYFI---------------------- 64

Qy      89 FPGCRTLAKYGQRQWKNKEDCWGTQELSCDLTSETSDIQEPYYGRVRAASAGSYSEWSMT 148
                  |||::| || :|       |||::|||| :  || :|:|      |:|: :
Db      65 ---------YGQKKWLNKSECRNINRTYCDLSAETSDYEHQYYAKVKAIWGTKCSKWAES 115

Qy     149 PRFTPWWETKIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYY-ELLYRVFII 207
            || |: ||:| || : :|    |: |:| ||    |  ::  ||::  |  | | | ::
Db     116 GRFYPFLETQIGPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQQIYSNLKYNVSVL 175

Qy     208 NNSLEKEQKVYEGAHRAVEIEALTPHSSYCVVAEIYQPMLDRRSQRSEERC 258
           |    :       |  | :  | |:: |||  | : |   ||:| ||::|
Db     176 NTKSNRTWSQCVTNHTLV-LTWLEPNTLYCVHVESFVPGPPRRAQPSEKQC 225
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RESULT 9
US-09-746-359A-54
; Sequence 54, Application US/09746359A
; Patent No. US20020042366A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Penny
; APPLICANT: Foster, Donald C.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Madden, Karen L.
; APPLICANT: Kelly, James D.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Blumberg, Hal
; APPLICANT: Eagan, Maribeth A.
; APPLICANT: Jaspers, Stephen R.
; APPLICANT: Chandrasekher, Yasmin A.
; APPLICANT: No. US20020042366A1ak, Julia E.
; TITLE OF INVENTION: Method for Treating Inflammation
; FILE REFERENCE: 99-108
; CURRENT APPLICATION NUMBER: US/09/746,359A
; CURRENT FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/171,969
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/213,341
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 54
; LENGTH: 547
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-746-359A-54

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  Query Match             21.7%;  Score 310;  DB 10;  Length 547;
  Best Local Similarity   32.0%;  Pred. No. 4.6e-22;
  Matches   74;  Conservative   33;  Mismatches   90;  Indels   34;  Gaps    3;

Qy      29 KPQRVQFQSRNFHNILQWQPGRALTGNSSVYFVQYKIMFSCSMKSSHQKPSGCWQHISCN 88
           ||  : | | |  |:||| |   | |    | ||| |
Db      10 KPANITFLSINMKNVLQWTPPEGLQGVKVTYTVQYFI---------------------- 46

Qy      89 FPGCRTLAKYGQRQWKNKEDCWGTQELSCDLTSETSDIQEPYYGRVRAASAGSYSEWSMT 148
                  |||::| || :|       |||::|||| :  || :|:|      |:|: :
Db      47 ---------YGQKKWLNKSECRNINRTYCDLSAETSDYEHQYYAKVKAIWGTKCSKWAES 97

Qy     149 PRFTPWWETKIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYY-ELLYRVFII 207
            || |: ||:| || : :|    |: |:| ||    |  ::  ||::  |  | | | ::
Db      98 GRFYPFLETQIGPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQQIYSNLKYNVSVL 157

Qy     208 NNSLEKEQKVYEGAHRAVEIEALTPHSSYCVVAEIYQPMLDRRSQRSEERC 258
           |    :        |  | :  | |:: |||  | : |   ||:| ||::|
Db     158 NTKSNRTWSQCVTNHTLV-LTWLEPNTLYCVHVESFVPGPPRRAQPSEKQC 207
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RESULT 10
US-09-746-359A-11
; Sequence 11, Application US/09746359A
; Patent No. US20020042366A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Penny
; APPLICANT: Foster, Donald C.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Madden, Karen L.
; APPLICANT: Kelly, James D.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Blumberg, Hal
; APPLICANT: Eagan, Maribeth A.
; APPLICANT: Jaspers, Stephen R.
; APPLICANT: Chandrasekher, Yasmin A.
; APPLICANT: No. US20020042366A1ak, Julia E.
; TITLE OF INVENTION: Method for Treating Inflammation
; FILE REFERENCE: 99-108
; CURRENT APPLICATION NUMBER: US/09/746,359A
; CURRENT FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/171,969
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/213,341
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 553
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-746-359A-11

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  Query Match             21.7%;  Score 310;  DB 10;  Length 553;
  Best Local Similarity   32.0%;  Pred. No. 4.7e-22;
  Matches   74;  Conservative   33;  Mismatches   90;  Indels   34;  Gaps    3;

Qy      29 KPQRVQFQSRNFHNILQWQPGRALTGNSSVYFVQYKIMFSCSMKSSHQKPSGCWQHISCN 88
           ||  : | | |  |:||| |   | |    | ||| |
Db      39 KPANITFLSINMKNVLQWTPPEGLQGVKVTYTVQYFI---------------------- 75

Qy      89 FPGCRTLAKYGQRQWKNKEDCWGTQELSCDLTSETSDIQEPYYGRVRAASAGSYSEWSMT 148
                  |||::| || :|       |||::|||| :  || :|:|      |:|: :
Db      76 ---------YGQKKWLNKSECRNINRTYCDLSAETSDYEHQYYAKVKAIWGTKCSKWAES 126

Qy     149 PRFTPWWETKIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYY-ELLYRVFII 207
            || |: ||:| || : :|    |: |:| ||    |  ::  ||::  |  | | | ::
Db     127 GRFYPFLETQIGPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQQIYSNLKYNVSVL 186

Qy     208 NNSLEKEQKVYEGAHRAVEIEALTPHSSYCVVAEIYQPMLDRRSQRSEERC 258
           |    :        |  | :  | |:: |||  | : |   ||:| ||::|
Db     187 NTKSNRTWSQCVTNHTLV-LTWLEPNTLYCVHVESFVPGPPRRAQPSEKQC 236
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RESULT 11
US-09-949-192-7
; Sequence 7, Application US/09949192
; Patent No. US20020142292A1
; GENERAL INFORMATION:
; APPLICANT: Parham, Christi L.
; APPLICANT: Gorman, Daniel L.
; APPLICANT: Kurata, Hirokazu
; APPLICANT: Arai, Naoko
; APPLICANT: Sana, Theodore R.
; APPLICANT: Mattson, Jeanine D.
; APPLICANT: Murphy, Erin E.
; APPLICANT: Savkoor, Chetan
; APPLICANT: Grein, Jeffery
; APPLICANT: Smith, Kathleen M.
; APPLICANT: McClanahan, Terrill K.
; TITLE OF INVENTION: MAMMALIAN GENES; RELATED REAGENTS AND METHODS
; FILE REFERENCE: DX01169K
; CURRENT APPLICATION NUMBER: US/09/949,192
; CURRENT FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: 60/231,267
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 553
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (522)..(522)
; OTHER INFORMATION: unknown amino
US-09-949-192-7

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  Query Match             21.7%;  Score 310;  DB 10;  Length 553;
  Best Local Similarity   32.0%;  Pred. No. 4.7e-22;
  Matches   74;  Conservative   33;  Mismatches   90;  Indels   34;  Gaps    3;

Qy      29 KPQRVQFQSRNFHNILQWQPGRALTGNSSVYFVQYKIMFSCSMKSSHQKPSGCWQHISCN 88
           ||  : | | |  |:||| |   | |    | ||| |
Db      39 KPANITFLSINMKNVLQWTPPEGLQGVKVTYTVQYFI---------------------- 75

Qy      89 FPGCRTLAKYGQRQWKNKEDCWGTQELSCDLTSETSDIQEPYYGRVRAASAGSYSEWSMT 148
                  |||::| || :|       |||::|||| :  || :|:|      |:|: :
Db      76 ---------YGQKKWLNKSECRNINRTYCDLSAETSDYEHQYYAKVKAIWGTKCSKWAES 126

Qy     149 PRFTPWWETKIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYY-ELLYRVFII 207
            || |: ||:| || : :|    |: |:| ||    |  ::  ||::  |  | | | ::
Db     127 GRFYPFLETQIGPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQQIYSNLKYNVSVL 186

Qy     208 NNSLEKEQKVYEGAHRAVEIEALTPHSSYCVVAEIYQPMLDRRSQRSEERC 258
           |    :        |  | :  | |:: |||  | : |   ||:| ||::|
Db     187 NTKSNRTWSQCVTNHTLV-LTWLEPNTLYCVHVESFVPGPPRRAQPSEKQC 236
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RESULT 12
US-09-746-359A-62
; Sequence 62, Application US/09746359A
; Patent No. US20020042366A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Penny
; APPLICANT: Foster, Donald C.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Madden, Karen L.
; APPLICANT: Kelly, James D.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Blumberg, Hal
; APPLICANT: Eagan, Maribeth A.
; APPLICANT: Jaspers, Stephen R.
; APPLICANT: Chandrasekher, Yasmin A.
; APPLICANT: No. US20020042366A1ak, Julia E.

```
;  TITLE OF INVENTION: Method for Treating Inflammation
;  FILE REFERENCE: 99-108
;  CURRENT APPLICATION NUMBER: US/09/746,359A
;  CURRENT FILING DATE:  2001-05-21
;  PRIOR APPLICATION NUMBER: 60/171,969
;  PRIOR FILING DATE: 1999-12-23
;  PRIOR APPLICATION NUMBER: 60/213,341
;  PRIOR FILING DATE: 2000-06-22
;  NUMBER OF SEQ ID NOS: 72
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 62
;   LENGTH: 559
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-746-359A-62

  Query Match             21.7%;  Score 310;  DB 10;  Length 559;
  Best Local Similarity   32.0%;  Pred. No. 4.7e-22;
  Matches   74;  Conservative   33;  Mismatches   90;  Indels   34;  Gaps    3;

Qy      29 KPQRVQFQSRNFHNILQWQPGRALTGNSSVYFVQYKIMFSCSMKSSHQKPSGCWQHISCN 88
           ||  : | | |  |:||| |   | |    | ||| |
Db      10 KPANITFLSINMKNVLQWTPPEGLQGVKVTYTVQYFI---------------------- 46

Qy      89 FPGCRTLAKYGQRQWKNKEDCWGTQELSCDLTSETSDIQEPYYGRVRAASAGSYSEWSMT 148
                 |||::| || :|       |||::|||| :  || :|:|      |:|: :
Db      47 ---------YGQKKWLNKSECRNINRTYCDLSAETSDYEHQYYAKVKAIWGTKCSKWAES 97

Qy     149 PRFTPWWETKIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYY-ELLYRVFII 207
           || |: ||:| || : :|    |: |:| ||    |  ::  ||::  |  | | | ::
Db      98 GRFYPFLETQIGPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQQIYSNLKYNVSVL 157

Qy     208 NNSLEKEQKVYEGAHRAVEIEALTPHSSYCVVAEIYQPMLDRRSQRSEERC 258
           |    :        |  | :  | |:: |||  | : |   ||:| ||::|
Db     158 NTKSNRTWSQCVTNHTLV-LTWLEPNTLYCVHVESFVPGPPRRAQPSEKQC 207


RESULT 13
US-09-746-359A-53
; Sequence 53, Application US/09746359A
; Patent No. US20020042366A1
; GENERAL INFORMATION:
;  APPLICANT: Thompson, Penny
;  APPLICANT:  Foster, Donald C.
;  APPLICANT:  Xu, Wenfeng
;  APPLICANT:  Madden, Karen L.
;  APPLICANT:  Kelly, James D.
;  APPLICANT:  Sprecher, Cindy A.
;  APPLICANT:  Blumberg, Hal
;  APPLICANT:  Eagan, Maribeth A.
;  APPLICANT:  Jaspers, Stephen R.
;  APPLICANT:  Chandrasekher, Yasmin A.
;  APPLICANT:  No. US20020042366A1ak, Julia E.
;  TITLE OF INVENTION: Method for Treating Inflammation
;  FILE REFERENCE: 99-108
;  CURRENT APPLICATION NUMBER: US/09/746,359A
;  CURRENT FILING DATE:  2001-05-21
;  PRIOR APPLICATION NUMBER: 60/171,969
;  PRIOR FILING DATE: 1999-12-23
;  PRIOR APPLICATION NUMBER: 60/213,341
;  PRIOR FILING DATE: 2000-06-22
;  NUMBER OF SEQ ID NOS: 72
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 53
;   LENGTH: 571
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-746-359A-53

  Query Match             21.7%;  Score 310;  DB 10;  Length 571;
  Best Local Similarity   32.0%;  Pred. No. 4.9e-22;
  Matches   74;  Conservative   33;  Mismatches   90;  Indels   34;  Gaps    3;

Qy      29 KPQRVQFQSRNFHNILQWQPGRALTGNSSVYFVQYKIMFSCSMKSSHQKPSGCWQHISCN 88
           ||  : | | |  |:||| |   | |    | ||| |
Db      34 KPANITFLSINMKNVLQWTPPEGLQGVKVTYTVQYFI---------------------- 70

Qy      89 FPGCRTLAKYGQRQWKNKEDCWGTQELSCDLTSETSDIQEPYYGRVRAASAGSYSEWSMT 148
                 |||::| || :|       |||::|||| :  || :|:|      |:|: :
Db      71 ---------YGQKKWLNKSECRNINRTYCDLSAETSDYEHQYYAKVKAIWGTKCSKWAES 121

Qy     149 PRFTPWWETKIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYY-ELLYRVFII 207
           || |: ||:| || : :|    |: |:| ||    |  ::  ||::  |  | | | ::
Db     122 GRFYPFLETQIGPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQQIYSNLKYNVSVL 181

Qy     208 NNSLEKEQKVYEGAHRAVEIEALTPHSSYCVVAEIYQPMLDRRSQRSEERC 258
           |    :        |  | :  | |:: |||  | : |   ||:| ||::|
Db     182 NTKSNRTWSQCVTNHTLV-LTWLEPNTLYCVHVESFVPGPPRRAQPSEKQC 231


RESULT 14
US-09-746-359A-23
; Sequence 23, Application US/09746359A
; Patent No. US20020042366A1
; GENERAL INFORMATION:
;  APPLICANT: Thompson, Penny
;  APPLICANT:  Foster, Donald C.
;  APPLICANT:  Xu, Wenfeng
;  APPLICANT:  Madden, Karen L.
;  APPLICANT:  Kelly, James D.
;  APPLICANT:  Sprecher, Cindy A.
;  APPLICANT:  Blumberg, Hal
;  APPLICANT:  Eagan, Maribeth A.
;  APPLICANT:  Jaspers, Stephen R.
;  APPLICANT:  Chandrasekher, Yasmin A.
;  APPLICANT:  No. US20020042366A1ak, Julia E.
;  TITLE OF INVENTION: Method for Treating Inflammation
;  FILE REFERENCE: 99-108
;  CURRENT APPLICATION NUMBER: US/09/746,359A
;  CURRENT FILING DATE:  2001-05-21
;  PRIOR APPLICATION NUMBER: 60/171,969
;  PRIOR FILING DATE: 1999-12-23
;  PRIOR APPLICATION NUMBER: 60/213,341
;  PRIOR FILING DATE: 2000-06-22
;  NUMBER OF SEQ ID NOS: 72
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 23
;   LENGTH: 594
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-746-359A-23

  Query Match             21.7%;  Score 310;  DB 10;  Length 594;
  Best Local Similarity   32.0%;  Pred. No. 5.1e-22;
  Matches   74;  Conservative   33;  Mismatches   90;  Indels   34;  Gaps    3;

Qy      29 KPQRVQFQSRNFHNILQWQPGRALTGNSSVYFVQYKIMFSCSMKSSHQKPSGCWQHISCN 88
           ||  : | | |  |:||| |   | |    | ||| |
Db      45 KPANITFLSINMKNVLQWTPPEGLQGVKVTYTVQYFI---------------------- 81

Qy      89 FPGCRTLAKYGQRQWKNKEDCWGTQELSCDLTSETSDIQEPYYGRVRAASAGSYSEWSMT 148
                 |||::| || :|       |||::|||| :  || :|:|      |:|: :
Db      82 ---------YGQKKWLNKSECRNINRTYCDLSAETSDYEHQYYAKVKAIWGTKCSKWAES 132

Qy     149 PRFTPWWETKIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYY-ELLYRVFII 207
           || |: ||:| || : :|    |: |:| ||    |  ::  ||::  |  | | | ::
Db     133 GRFYPFLETQIGPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQQIYSNLKYNVSVL 192

Qy     208 NNSLEKEQKVYEGAHRAVEIEALTPHSSYCVVAEIYQPMLDRRSQRSEERC 258
           |    :        |  | :  | |:: |||  | : |   ||:| ||::|
Db     193 NTKSNRTWSQCVTNHTLV-LTWLEPNTLYCVHVESFVPGPPRRAQPSEKQC 242


RESULT 15
US-09-864-761-40289
; Sequence 40289, Application US/09864761
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; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 40289
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL158138.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.5
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.8
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.5
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.3
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.9
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.7
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.3
; OTHER INFORMATION: SWISSPROT HIT: O28438, EVALUE 1.20e+00
; OTHER INFORMATION: EST_HUMAN HIT: AV714177.1, EVALUE 4.00e-26
US-09-864-761-40289

Query Match 20.3%; Score 289; DB 10; Length 56;
Best Local Similarity 100.0%; Pred. No. 2.4e-21;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 158 KIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYYELLYRVFIINNSLEK 213
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 1 KIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYYELLYRVFIINNSLEK 56

Search completed: December 22, 2002, 10:21:48
Job time : 22 secs

GenCore version 5.1.3

OM protein - protein search, using sw model

Run on: December 22, 2002, 10:06:17 ; Search time 80 Seconds
(without alignments)
674.804 Million cell updates/sec

Title: US-09-964-994-2
Perfect score: 1427
Sequence: 1 MPKHCFLGFLISFFLTGVAG.....YQPMLDRRSQRSEERCVEIP 262

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1427	100.0	263	4	Q969J5	Q969j5 homo sapien
2	1213	85.0	231	4	Q96A41	Q96a41 homo sapien
3	664	46.5	130	4	Q96QR0	Q96qr0 homo sapien
4	310	21.7	553	4	Q9UHF4	Q9uhf4 homo sapien
5	310	21.7	553	4	Q96SH8	Q96sh8 homo sapien
6	262	18.4	209	4	Q96SH7	Q96sh7 homo sapien
7	240	16.8	574	4	Q9HB22	Q9hb22 homo sapien
8	187.5	13.1	569	11	Q99ND6	Q99nd6 rattus norv
9	180.5	12.6	341	13	Q9YGC8	Q9ygc8 gallus gall
10	173.5	12.2	294	13	Q90W13	Q90w13 oncorhynchu
11	155.5	10.9	569	13	Q9YHW0	Q9yhw0 gallus gall
12	152.5	10.7	442	13	Q9PVJ9	Q9pvj9 gallus gall
13	149.5	10.5	325	4	Q9BUU4	Q9buu4 homo sapien
14	149	10.4	351	11	Q8VHM7	Q8vhm7 mus musculu
15	136.5	9.6	557	4	Q8WTZ2	Q8wtz2 homo sapien
16	126	8.8	294	11	Q8R3Q1	Q8r3q1 mus musculu
17	121.5	8.5	508	13	Q9YHV9	Q9yhv9 gallus gall
18	119.5	8.4	508	13	Q9PVK0	Q9pvk0 gallus gall
19	118.5	8.3	489	4	Q9BY69	Q9by69 homo sapien
20	115.5	8.1	332	6	Q9GK86	Q9gk86 ovis aries
21	110.5	7.7	332	11	Q63953	Q63953 mus musculu
22	108	7.6	484	4	Q14936	Q14936 homo sapien
23	101.5	7.1	239	4	Q15467	Q15467 homo sapien
24	101.5	7.1	331	4	Q9BUA0	Q9bua0 homo sapien
25	100.5	7.0	608	6	Q9N0Y7	Q9n0y7 monodelphis
26	95	6.7	1253	12	Q9JGK8	Q9jgk8 sagiyama vi
27	93	6.5	453	16	Q9K434	Q9k434 streptomyce
28	92.5	6.5	1155	17	Q8TPZ8	Q8tpz8 methanosarc
29	91.5	6.4	424	11	Q91YA2	Q91ya2 mus musculu
30	88	6.2	745	10	Q94LQ3	Q94lq3 oryza sativ
31	88	6.2	795	11	Q9CRF5	Q9crf5 mus musculu
32	88	6.2	2320	5	Q9XYM9	Q9xym9 trichomonas
33	87.5	6.1	674	13	Q90369	Q90369 coturnix co
34	87.5	6.1	675	13	Q9PSH7	Q9psh7 gallus gall
35	87.5	6.1	2959	11	Q9JIF1	Q9jif1 rattus norv
36	87	6.1	304	4	Q9Y5Q4	Q9y5q4 homo sapien
37	87	6.1	1145	12	Q87049	Q87049 semliki for
38	87	6.1	1244	12	Q88628	Q88628 chikungunya
39	87	6.1	1384	4	O75257	O75257 homo sapien
40	86.5	6.1	392	11	Q99KP5	Q99kp5 mus musculu
41	86.5	6.1	632	6	Q95ML5	Q95ml5 saimiri bol
42	86.5	6.1	1083	5	Q9W071	Q9w071 drosophila
43	86.5	6.1	1289	4	Q9Y2A5	Q9y2a5 homo sapien
44	86	6.0	477	11	Q91Y85	Q91y85 mus musculu
45	85.5	6.0	1002	15	Q9IMZ9	Q9imz9 human immun

ALIGNMENTS

RESULT 1
Q969J5
ID Q969J5 PRELIMINARY; PRT; 263 AA.
AC Q969J5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Soluble cytokine class II receptor, long isoform precursor
DE (Interleukin 22-binding protein CRF2-10L).
GN CRF2-S1 OR IL22BP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RX MEDLINE=21518574; PubMed=11607789;
RA Gruenberg B.H., Schoenemeyer A., Weiss B., Toschi L., Kunz S.,
RA Wolk K., Asadullah K., Sabat R.;
RT "A novel, soluble homologue of the human IL-10 receptor with
RT preferential expression in placenta.";
RL Genes Immun. 2:329-334(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21286453; PubMed=11390454;
RA Kotenko S.V., Izotova L.S., Mirochnitchenko O.V., Esterova E.,
RA Dickensheets H., Donnelly R.P., Pestka S.;
RT "Identification, cloning, and characterization of a novel soluble
RT receptor that binds IL-22 and neutralizes its activity.";
RL J. Immunol. 166:7096-7103(2001).
DR EMBL; AJ313162; CAC85635.1; -.
DR EMBL; AY040567; AAK85715.1; -.
DR InterPro; IPR000282; Cytok_receptor_2.
KW Receptor; Signal.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 263 SOLUBLE CYTOKINE CLASS II RECEPTOR, LONG
FT ISOFORM.
SQ SEQUENCE 263 AA; 30550 MW; C96ECEC5D78AC79B CRC64;

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  Query Match           100.0%;  Score 1427;  DB 4;  Length 263;
  Best Local Similarity  100.0%;  Pred. No. 2.4e-129;
  Matches  262;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MPKHCFLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVYF 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2 MPKHCFLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVYF 61

Qy      61 VQYKIMFSCSMKSSHQKPSGCWQHISCNFPGCRTLAKYGQRQWKNKEDCWGTQELSCDLT 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      62 VQYKIMFSCSMKSSHQKPSGCWQHISCNFPGCRTLAKYGQRQWKNKEDCWGTQELSCDLT 121

Qy     121 SETSDIQEPYYGRVRAASAGSYSEWSMTPRFTPWWETKIDPPVMNITQVNGSLLVILHAP 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     122 SETSDIQEPYYGRVRAASAGSYSEWSMTPRFTPWWETKIDPPVMNITQVNGSLLVILHAP 181

Qy     181 NLPYRYQKEKNVSIEDYYELLYRVFIINNSLEKEQKVYEGAHRAVEIEALTPHSSYCVVA 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     182 NLPYRYQKEKNVSIEDYYELLYRVFIINNSLEKEQKVYEGAHRAVEIEALTPHSSYCVVA 241

Qy     241 EIYQPMLDRRSQRSEERCVEIP 262
           |||||||||||||||||||||||
Db     242 EIYQPMLDRRSQRSEERCVEIP 263
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RESULT 2
Q96A41
ID   Q96A41      PRELIMINARY;      PRT;   231 AA.
AC   Q96A41;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Soluble cytokine class II receptor, short isoform precursor
DE   (Interleukin 22-binding protein CRF2-10) (Class II cytokine receptor)
DE   (Interleukin-22 binding protein).
GN   CRF2-S1 OR IL22BP OR IL22RA2 OR IL-22BP.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=MAMMARY GLAND;
RX   MEDLINE=21518574; PubMed=11607789;
RA   Gruenberg B.H., Schoenemeyer A., Weiss B., Toschi L., Kunz S.,
RA   Wolk K., Asadullah K., Sabat R.;
RT   "A novel, soluble homologue of the human IL-10     receptor with
RT   preferential expression in placenta.";
RL   Genes Immun. 2:329-334(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21286453; PubMed=11390454;
RA   Kotenko S.V., Izotova L.S., Mirochnitchenko O.V., Esterova E.,
RA   Dickensheets H., Donnelly R.P., Pestka S.;
RT   "Identification, cloning, and characterization of a novel soluble
RT   receptor that binds IL-22 and neutralizes its activity.";
RL   J. Immunol. 166:7096-7103(2001).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21396522; PubMed=11481447;
RA   Xu W., Presnell S.R., Parrish-Novak J., Kindsvogel W., Jaspers S.,
RA   Chen Z., Dillon S.R., Gao Z., Gilbert T., Madden K., Schlutsmeyer S.,
RA   Yao L., Whitmore T.E., Chandrasekher Y., Grant F.J., Maurer M.,
RA   Jelinek L., Storey H., Brender T., Hammond A., Topouzis S.,
RA   Clegg C.H., Foster D.C.;
RT   "A soluble class II cytokine receptor, IL-22RA2, is a naturally
RT   occurring IL-22 antagonist.";
RL   Proc. Natl. Acad. Sci. U.S.A. 98:9511-9516(2001).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BREAST;
RA   Dumoutier L., Lejeune D., Renauld J.C.;
RT   "Cloning and characterization of Interelukin-22 Binding Protein (IL-
RT   22BP), a natural antagonist of IL-TIF/IL-22.";
RL   Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ313161; CAC85634.1; -.
DR   EMBL; AY040566; AAK85714.1; -.
DR   EMBL; AY044429; AAK91775.1; -.
DR   EMBL; AJ297262; CAC83097.1; -.
DR   InterPro; IPR000282; Cytok_receptor_2.
KW   Receptor; Signal.
FT   SIGNAL        1     21       POTENTIAL.
FT   CHAIN        22    231       SOLUBLE CYTOKINE CLASS II RECEPTOR, SHORT
FT                                ISOFORM.
SQ   SEQUENCE   231 AA;  26979 MW;  24A6912BFF75100F CRC64;
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  Query Match           85.0%;  Score 1213;  DB 4;  Length 231;
  Best Local Similarity  87.8%;  Pred. No. 8.3e-109;
  Matches  230;  Conservative    0;  Mismatches    0;  Indels   32;  Gaps    1;

Qy       1 MPKHCFLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVYF 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2 MPKHCFLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVYF 61

Qy      61 VQYKIMFSCSMKSSHQKPSGCWQHISCNFPGCRTLAKYGQRQWKNKEDCWGTQELSCDLT 120
           |||||                                 ||||||||||||||||||||||
Db      62 VQYKI---------------------------------YGQRQWKNKEDCWGTQELSCDLT 89

Qy     121 SETSDIQEPYYGRVRAASAGSYSEWSMTPRFTPWWETKIDPPVMNITQVNGSLLVILHAP 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      90 SETSDIQEPYYGRVRAASAGSYSEWSMTPRFTPWWETKIDPPVMNITQVNGSLLVILHAP 149

Qy     181 NLPYRYQKEKNVSIEDYYELLYRVFIINNSLEKEQKVYEGAHRAVEIEALTPHSSYCVVA 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     150 NLPYRYQKEKNVSIEDYYELLYRVFIINNSLEKEQKVYEGAHRAVEIEALTPHSSYCVVA 209

Qy     241 EIYQPMLDRRSQRSEERCVEIP 262
           |||||||||||||||||||||||
Db     210 EIYQPMLDRRSQRSEERCVEIP 231
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RESULT 3
Q96QR0
ID   Q96QR0      PRELIMINARY;      PRT;   130 AA.
AC   Q96QR0;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Interleukin 22-binding protein CRF2-10S.
GN   IL22BP.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21286453; PubMed=11390454;
RA   Kotenko S.V., Izotova L.S., Mirochnitchenko O.V., Esterova E.,
RA   Dickensheets H., Donnelly R.P., Pestka S.;
RT   "Identification, cloning, and characterization of a novel soluble
RT   receptor that binds IL-22 and neutralizes its activity.";
RL   J. Immunol. 166:7096-7103(2001).
DR   EMBL; AY040568; AAK85716.1; -.
DR   InterPro; IPR000282; Cytok_receptor_2.
SQ   SEQUENCE   130 AA;  15128 MW;  A165814C641F5E5B CRC64;
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  Query Match           46.5%;  Score 664;  DB 4;  Length 130;
  Best Local Similarity  79.5%;  Pred. No. 3.2e-56;
  Matches  124;  Conservative    0;  Mismatches    0;  Indels   32;  Gaps    1;

Qy       1 MPKHCFLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVYF 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2 MPKHCFLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVYF 61

Qy      61 VQYKIMFSCSMKSSHQKPSGCWQHISCNFPGCRTLAKYGQRQWKNKEDCWGTQELSCDLT 120
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          |||||                                 ||||||||||||||||||||||
Db      62 VQYKI-------------------------------YGQRQWKNKEDCWGTQELSCDLT 89

Qy     121 SETSDIQEPYYGRVRAASAGSYSEWSMTPRFTPWWE 156
           ||||||||||||||||||||||||||||||||||||
Db      90 SETSDIQEPYYGRVRAASAGSYSEWSMTPRFTPWWE 125


RESULT 4
Q9UHF4
ID   Q9UHF4      PRELIMINARY;      PRT;   553 AA.
AC   Q9UHF4;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Class II cytokine receptor ZCYTOR7.
GN   ZCYTOR7.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
     NCBI_TaxID=9606;
     [1]
RP   SEQUENCE FROM N.A.
RA   Lok S., Kho C., Jelmberg A., Adams R., Whitmore T., Farrah T.,
RA   O'Hara P.;
RT   "Homo sapiens cytokine receptor homolog.";
RL   Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Presnell S., Gilbert T., Whitmore T., Foster D., Hart C., Lehner J.,
RA   Martinez T., Hoffman R., O'Hara P.;
RL   Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF184971; AAF01320.1; -.
DR   HSSP; P13726; 2HFT.
DR   InterPro; IPR000282; Cytok_receptor_2.
DR   InterPro; IPR001187; Tissue_factor.
DR   Pfam; PF01108; Tissue_fac; 1.
KW   Receptor.
SQ   SEQUENCE   553 AA;  62533 MW;  7C23C8543B114659 CRC64;

  Query Match             21.7%;  Score 310;  DB 4;  Length 553;
  Best Local Similarity   32.0%;  Pred. No. 2.2e-21;
  Matches   74;  Conservative   33;  Mismatches   90;  Indels   34;  Gaps    3;

Qy      29 KPQRVQFQSRNFHNILQWQPGRALTGNSSVYFVQYKIMFSCSMKSSHQKPSGCWQHISCN 88
           ||  : | | |  |:||| |   | |    | ||| |
Db      39 KPANITFLSINMKNVLQWTPPEGLQGVKVTYTVQYFI---------------------- 75

Qy      89 FPGCRTLAKYGQRQWKNKEDCWGTQELSCDLTSETSDIQEPYYGRVRAASAGSYSEWSMT 148
                 |||::| || :|       |||::|||| :  || :|:|      |:|: :
Db      76 ---------YGQKKWLNKSECRNINRTYCDLSAETSDYEHQYYAKVKAIWGTKCSKWAES 126

Qy     149 PRFTPWWETKIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYY-ELLYRVFII 207
            || |: ||:| || : :|    |: |:| ||    |  ::  ||::  |  | | | ::
Db     127 GRFYPFLETQIGPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQQIYSNLKYNVSVL 186

Qy     208 NNSLEKEQKVYEGAHRAVEIEALTPHSSYCVVAEIYQPMLDRRSQRSEERC 258
           |    :       |  | :  | |:: |||  | : |   ||:| ||::|
Db     187 NTKSNRTWSQCVTNHTLV-LTWLEPNTLYCVHVESFVPGPPRRAQPSEKQC 236


RESULT 5
Q96SH8
ID   Q96SH8      PRELIMINARY;      PRT;   553 AA.
AC   Q96SH8;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   BA204P2.1.1 (interleukin 20 receptor alpha, isoform 1).
GN   IL20RA.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Griffiths C.;
RL   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AL135902; CAC38375.1; -.
DR   InterPro; IPR000282; Cytok_receptor_2.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR001187; Tissue_factor.
DR   Pfam; PF01108; Tissue_fac; 1.
DR   SMART; SM00060; FN3; 1.
KW   Receptor.
SQ   SEQUENCE   553 AA;  62485 MW;  D5C2621FDC848328 CRC64;

  Query Match             21.7%;  Score 310;  DB 4;  Length 553;
  Best Local Similarity   32.0%;  Pred. No. 2.2e-21;
  Matches   74;  Conservative   33;  Mismatches   90;  Indels   34;  Gaps    3;

Qy      29 KPQRVQFQSRNFHNILQWQPGRALTGNSSVYFVQYKIMFSCSMKSSHQKPSGCWQHISCN 88
           ||  : | | |  |:||| |   | |    | ||| |
Db      39 KPANITFLSINMKNVLQWTPPEGLQGVKVTYTVQYFI---------------------- 75

Qy      89 FPGCRTLAKYGQRQWKNKEDCWGTQELSCDLTSETSDIQEPYYGRVRAASAGSYSEWSMT 148
                 |||::| || :|       |||::|||| :  || :|:|      |:|: :
Db      76 ---------YGQKKWLNKSECRNINRTYCDLSAETSDYEHQYYAKVKAIWGTKCSKWAES 126

Qy     149 PRFTPWWETKIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYY-ELLYRVFII 207
            || |: ||:| || : :|    |: |:| ||    |  ::  ||::  |  | | | ::
Db     127 GRFYPFLETQIGPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQQIYSNLKYNVSVL 186

Qy     208 NNSLEKEQKVYEGAHRAVEIEALTPHSSYCVVAEIYQPMLDRRSQRSEERC 258
           |    :       |  | :  | |:: |||  | : |   ||:| ||::|
Db     187 NTKSNRTWSQCVTNHTLV-LTWLEPNTLYCVHVESFVPGPPRRAQPSEKQC 236


RESULT 6
Q96SH7
ID   Q96SH7      PRELIMINARY;      PRT;   209 AA.
AC   Q96SH7;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   BA204P2.1.3 (interleukin 20 receptor alpha, isoform 3).
GN   IL20RA.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Griffiths C.;
RL   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AL135902; CAC38376.1; -.
DR   InterPro; IPR000282; Cytok_receptor_2.
KW   Receptor.
SQ   SEQUENCE   209 AA;  23616 MW;  467AB77BE3840361 CRC64;

  Query Match             18.4%;  Score 262;  DB 4;  Length 209;
  Best Local Similarity   31.1%;  Pred. No. 2.9e-17;
  Matches   61;  Conservative   29;  Mismatches   72;  Indels   34;  Gaps    3;

Qy      29 KPQRVQFQSRNFHNILQWQPGRALTGNSSVYFVQYKIMFSCSMKSSHQKPSGCWQHISCN 88
           ||  : | | |  |:||| |   | |    | ||| |
Db      39 KPANITFLSINMKNVLQWTPPEGLQGVKVTYTVQYFI---------------------- 75

Qy      89 FPGCRTLAKYGQRQWKNKEDCWGTQELSCDLTSETSDIQEPYYGRVRAASAGSYSEWSMT 148
                 |||::| || :|       |||::|||| :  || :|:|      |:|: :
Db      76 ---------YGQKKWLNKSECRNINRTYCDLSAETSDYEHQYYAKVKAIWGTKCSKWAES 126

Qy     149 PRFTPWWETKIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYY-ELLYRVFII 207
            || |: ||:| || : :|    |: |:| ||    |  ::  ||::  |  | | | ::
Db     127 GRFYPFLETQIGPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQQIYSNLKYNVSVL 186
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Qy     208 NNSLEKEQKV-YEGAH 222
           |    :   : : ||:
Db     187 NTKSNRTVSLKWNGAY 202
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RESULT 7
Q9HB22
ID   Q9HB22   PRELIMINARY;   PRT;   574 AA.
AC   Q9HB22;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   IL-22 receptor.
GN   IL22R.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
[redacted] SEQUENCE FROM N.A.
[redacted] MEDLINE=20469498; PubMed=10875937;
[redacted] Xie M.H., Aggarwal S., Ho W.H., Foster J., Zhang Z., Stinson J.,
RA   Wood W.I., Goddard A.D., Gurney A.L.;
RT   "Interleukin (IL)-22, a Novel Human Cytokine That Signals through the
RT   Interferon Receptor-related Proteins CRF2-4 and IL-22R.";
RL   J. Biol. Chem. 275:31335-31339(2000).
DR   EMBL; AF286095; AAG22073.1; -.
DR   HSSP; P13726; 1TFH.
DR   InterPro; IPR000282; Cytok_receptor_2.
KW   Receptor.
SQ   SEQUENCE   574 AA; 62977 MW; C179C7085C6F3420 CRC64;

  Query Match   16.8%; Score 240; DB 4; Length 574;
  Best Local Similarity   28.6%; Pred. No. 1.3e-14;
  Matches   69; Conservative   31; Mismatches   93; Indels   48; Gaps   6;

```
Qy      20 GTQSTHESLKP----QRVQFQSRNFHNILQWQPGRALTGNSSVYFVQYKIMFSCSMKSSH 75
           |: : |    |    | |:||| || ||| |  |    | : :|| ::||
Db      11 GSLAAHAPEDPSDLLQHVKFQSSNFENILTWDSGPEGTPD-TVYSIEYK---------- 58

Qy      76 QKPSGCWQHISCNFPGCRTLAKYGQRQWKNKEDCWGTQELSCDLTSETSDIQEPYYGRVR 135
                                  ||:| |  |: |      ||:|| || :: | || ||
Db      59 --------------------TYGERDWVAKKGCQRITRKSCNLTVETGNLTELYYARVT 97

Qy     136 AASAGSYSEWSMTPRFTPWWETKIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIE 195
           | |||  |   || ||:    | : || :       |: :|:|    | |      :::|
Db      98 AVSAGGRSATKMTDRFSSLQHTTLKPPDVTCISKVRSIQMIVHPTPTPIRAGDGHRLTLE 157

Qy     196 D-YYELLYRVFIINNSLEKEQKVYE----GAHRAVEIEALTPHSSYCVVAEIYQPMLDRR 250
           | :::| | : :  |      : |:    |  |  |   ||| : :     |  |   :
Db     158 DIFHDLFYHLELQVN------RTYQMHLGGKQREYEFFGLTPDTEFLGTIMICVPTWAKE 211

Qy     251 S 251
           |
Db     212 S 212
```

RESULT 8
Q99ND6
ID   Q99ND6   PRELIMINARY;   PRT;   569 AA.
AC   Q99ND6;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Interleukin-10 receptor, alpha chain precursor.
GN   IL-10RA.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PERIPHERAL BLOOD;
RA   Ward H., Vigues S., Poole S., Bristow A.F.;
RT   "The rat interleukin-10 receptor: cloning and sequencing of cDNA
RT   coding for the alpha-chain protein sequence, and demonstration by
RT   Western blotting of expression in ratbrain.";
RL   Cytokine 0:0-0(0).
DR   EMBL; AJ305049; CAC24567.1; -.
DR   InterPro; IPR000282; Cytok_receptor_2.
KW   Receptor; Signal.
FT   SIGNAL   1   16   POTENTIAL.
FT   CHAIN   17   569   INTERLEUKIN-10 RECEPTOR.
SQ   SEQUENCE   569 AA; 63526 MW; 2354FD61DB351BD2 CRC64;

  Query Match   13.1%; Score 187.5; DB 11; Length 569;
  Best Local Similarity   25.1%; Pred. No. 1.4e-09;
  Matches   70; Conservative   35; Mismatches   93; Indels   81; Gaps   12;

```
Qy       7 LGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQ--PGRALTGNSSVYFVQYK 64
           | ||:|     :       |   |  | |::| | :||:|   | :    : | |   |:
Db       6 LPFLVSISSLSLGFRAHGTELPSPSSVWFEARFFQHILRWMSIPNQ----SESTY---YE 58

Qy      65 IMFSCSMKSSHQKPSGCWQHISCNFPGCRTLAKYGQRQWKNKEDCWGTQELSCDLTSETS 124
           :                                | |||   ||:   |   | ||||||: |
Db      59 V----------------------------ALKKYGTSIWKDIHICSKAQTLSCDLTTSTL 90

Qy     125 DI--QEPYYGRVRAASAGSYSEWSMT-PRFTPWWETKIDPPVMNITQV-----NGSLLVI 176
           |:     |  ||||     || |::|  |||      :|  :: :  |     || :
Db      91 DLYHSSGYRARVRAVDNSQYSNWTITETRFT------VDEVILTVDSVTVKVSNGFIYGT 144

Qy     177 LHAPNLPYRYQKEKNVSIEDYYE------LLYRVFI--------INNSLEKEQKVYEGAH 222
           :| |        :   | : | ||       :||| |        |  ::|:|    |
Db     145 IHPP-------RPNLVPVGDEYEQIFTHHRIYRVCIRKFSEQKNITKTVEQENFTLEVPK 197

Qy     223 RAVEIEALTPHSSYCVVAEIYQPMLDRRSQRSEERCVEI 261
           |           :||    :      ::: |||:|: :
Db     198 RM---------RKFCVKVMPHVESRINKAEWSEEQCLHV 227
```

RESULT 9
Q9YGC8
ID   Q9YGC8   PRELIMINARY;   PRT;   341 AA.
AC   Q9YGC8;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Interleukin-10 receptor 2.
GN   IL10R2.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Reboul J., Gardiner K., Monneron D., Uze G., Lutfalla G.;
RT   "Comparative genomic analysis of the interferon/interleukin-10
RT   receptor gene cluster.";
RL   Genome Res. 0:0-0(1999).
DR   EMBL; AF082667; AAD13678.1; -.
DR   EMBL; AF082666; AAD13671.1; -.
DR   HSSP; P13726; 1AHW.
DR   InterPro; IPR000282; Cytok_receptor_2.
DR   InterPro; IPR001187; Tissue_factor.
DR   Pfam; PF01108; Tissue_fac; 1.
DR   PRINTS; PR00346; TISSUEFACTOR.
KW   Receptor.
SQ   SEQUENCE   341 AA; 39062 MW; 18027239BF8A9C87 CRC64;

  Query Match   12.6%; Score 180.5; DB 13; Length 341;
  Best Local Similarity   24.2%; Pred. No. 3.7e-09;
  Matches   56; Conservative   37; Mismatches   97; Indels   41; Gaps   7;

```
Qy      29 KPQRVQFQSRNFHNILQWQPGRALTGNSSVYFVQYKIMFSCSMKSSHQKPSGCWQHISCN 88
           ||:  :  | || ::| | |     || | | || | :|         |   : ::: |
```

```
Db      23 KPRNARISSVNFRSVLLWDPPGVRKGNLS-YTVQAKSIF----------PKQNFNNVTTN 71

Qy      89 FPGCRTLAKYGQRQWKNKEDCWGTQELSCDLTSETSDIQEPYYGRVRAASAGSYSEWSMT 148
                                  ||::|    :   |  |||      :|:|::
Db      72 L----------------------NVTECDVSS--LSVYGAYVLRVRTEWEDEHSDWAVV 106

Qy     149 PRFTPWWETKIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYY-ELLYRVFII 207
            || |  :| | || :|:   :|:| |    |     : |    |:: ||   :||:
Db     107 -RFKPMADTVIGPPSVNVKSESGTLHVDFTGPAADREHDK---WSLKQYYGSWIYRILYW 162

Qy     208 NNSLEKEQKVYEGAHRAVEIEALTPHSSYCVVAEIYQPMLDRRSQRSEERC 258
               |:    :  | :  :  | | : ||:  :   |  ::  :||:| |
Db     163 KKGSNKKVIHIDTKHNSEILSQLEPWTIYCIQVQGVIPEWNKTGERSQELC 213
```

RESULT 10
Q90W13
ID Q90W13 PRELIMINARY; PRT; 294 AA.
AC Q90W13;
    01-DEC-2001 (TrEMBLrel. 19, Created)
    01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
    01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Tissue factor precursor.
GN TF.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=HEAD KIDNEY;
RA Sangrador-Vegas A., Smith T.J.;
RT "Molecular cloning of rainbow trout (Oncorhynchus mykiss)tissue factor
RT precursor by use of suppression subtractive hybridisation.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AJ295167; CAC82787.1; -.
DR InterPro; IPR000282; Cytok_receptor_2.
DR InterPro; IPR001187; Tissue_factor.
DR Pfam; PF01108; Tissue_fac; 1.
KW Signal.
FT SIGNAL   1   25   POTENTIAL.
FT CHAIN   26   294   TISSUE FACTOR.
SQ SEQUENCE   294 AA; 33404 MW; 105DDDA107E54EDE CRC64;

  Query Match   12.2%; Score 173.5; DB 13; Length 294;
  Best Local Similarity   26.8%; Pred. No. 1.5e-08;
  Matches   74; Conservative   34; Mismatches   91; Indels   77; Gaps   14;

```
Qy       8 GFLIS--FFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVYFVQYKI 65
            | |:|    |  | ||     |::    ||: | ||  || | |        : |   | :
Db      11 GVLLSSVLFTIGAAGEDYFPEAMD---VQWVSNNFKTILTWGP------EPTNY--TYTV 59

Qy      66 MFSCSMKSSHQKPSGCWQHISCNFPGCRTLAKYGQRQWKNKEDCWGTQELSCDLTSETSD 125
            ||   |   : |                                  |  :    ||||:|  :
Db      60 EFSRVGKDRQRNP---------------------------HCIRSSRTECDLTNELRN 90

Qy     126 IQEPYYGRVRAASAGSYSE------------WSMTPRFTPWWETKIDPPVMNITQVNGS 172
           :|| |        ||   ||             ::   ||:|:  |||  |   | |
Db      91 LQETY-------SADILSEPLPGVTSDLVEFPYTRAERFSPYKHTKIGGPAFKIVQSEDK 143

Qy     173 LLVILHAPN-LPYRYQKEKNVSIEDYY--ELLYRVFIIN--NSLEKEQKVYEGAHRAVEI 227
             : ||  : |   |: :: ::| | :  :| ||| | |   |  |::|: :   | ||:
Db     144 TKMTLHIQDPLTPLYKDDQLLTIRDIFKSDLKYRV-IYNKAGSTGKKEKMSD--LRDVEL 200

Qy     228 EALTPHSSYCVVAEIYQPMLDRRSQR-----SEERC 258
             |    ||||:   | |   | :|:     |: :|
Db     201 TNLDKGQSYCVIVAAYIP--SRSAQKRLGDWSKAQC 234
```

RESULT 11
Q9YHW0
ID Q9YHW0 PRELIMINARY; PRT; 569 AA.
AC Q9YHW0;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Interferon alpha/beta receptor 1.
GN IFNAR1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE=99177346; PubMed=10077530;
RA Reboul J., Gardiner K., Monneron D., Uze G., Lutfalla G.;
RT "Comparative genomic analysis of the Interferon/Interleukin-10
RT receptor gene cluster.";
RL Genome Res. 9:242-250(1999).
DR EMBL; AF082664; AAD13669.1; -.
DR InterPro; IPR000282; Cytok_receptor_2.
DR InterPro; IPR003961; FN_III.
DR SMART; SM00060; FN3; 1.
KW Receptor.
SQ SEQUENCE   569 AA; 64055 MW; 6A757DDFB891E605 CRC64;

  Query Match   10.9%; Score 155.5; DB 13; Length 569;
  Best Local Similarity   23.2%; Pred. No. 1.7e-06;
  Matches   63; Conservative   38; Mismatches   101; Indels   69; Gaps   12;

```
Qy       2 PKHCFLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSV-YF 60
             | ||             :  |:  :: | |  |:  : |    | |        |  | |
Db     224 PIHC-----------IKTTRKVNDLLCPTNVRVFALNMKFYLLWDNHY----NEHVTYT 267

Qy      61 VQYKIMFSCSMKSSHQKPSGCWQHISCNFPGCRTLAKYGQRQWKNKEDCWGTQELSCDLT 120
           |||   :   :|: :   |  || :|    ||  :                    : |:|:
Db     268 VQYLTGY---LKNLYDDYSSKWQKVS----GCENIT---------------SMKCNLS 303

Qy     121 SETSDIQEPYYGRVRAASAGSYSEWSMTPRFTPWWETKIDPPVMN---------ITQVN 170
           |        || ||:| :   ||:  ::       : ::|||| |         |:
Db     304 SVIKPTSASYYFRVQAMN--EYSKSCLSK------DVEVDPPVTNEIGPPDVKVDISD-- 353

Qy     171 GSLLVILHAPNLPYRYQKEKNVSIEDYYELLYRVFIINNSL--EKEQKVYEGAHRAVEIE 228
             |:||    |      | :|  | |:  |::    ||   |:| |: |       :
Db     354 ----VLLHIKITPPGGPGNKIMS--DLYDFSYQILYWKNSSDNEEEVKMKETKQTIATVS 407

Qy     229 ALTPHSSYCVVAEIYQPMLDRRSQRSEERCV 259
             | | : |||  : :    :: |  | | |:
Db     408 DLAPSTLYCVKVQAFSEAYNKSSDFSREECI 438
```

RESULT 12
Q9PVJ9
ID Q9PVJ9 PRELIMINARY; PRT; 442 AA.
AC Q9PVJ9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Interferon alpha/beta receptor 1 (Fragment).
GN IFNAR1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99177346; PubMed=10077530;
RA Reboul J., Gardiner K., Monneron D., Uze G., Lutfalla G.;
RT "Comparative genomic analysis of the Interferon/Interleukin-10
RT receptor gene cluster.";
RL Genome Res. 9:242-250(1999).
DR EMBL; AF082667; AAD13679.1; -.

```
DR   InterPro; IPR000282; Cytok_receptor_2.
DR   InterPro; IPR003961; FN_III.
DR   SMART; SM00060; FN3; 1.
KW   Receptor.
FT   NON_TER     442    442
SQ   SEQUENCE   442 AA;  49877 MW;  839EBE92170609E0 CRC64;

  Query Match             10.7%;  Score 152.5;  DB 13;  Length 442;
  Best Local Similarity   22.9%;  Pred. No. 2.5e-06;
  Matches   62;  Conservative   39;  Mismatches  101;  Indels   69;  Gaps   12;

Qy       2 PKHCFLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSV-YF 60
           | ||            :  |:  :: | |  |:  : |    | |        |  | |
Db     224 PIHC-----------IKTTRKVNDLLCPTNVRVFALNMKFYLLWDNHY----NEHVTYT 267

Qy      61 VQYKIMFSCSMKSSHQKPSGCWQHISCNFPGCRTLAKYGQRQWKNKEDCWGTQELSCDLT 120
           |||   :   :|: :   |  || :|    ||  :                  : |:|:
Db     268 VQYLTGY---LKNLYDDYSSKWQKVS----GCENIT----------------SMKCNLS 303

Qy     121 SETSDIQEPYYGRVRAASAGSYSEWSMTPRFTPWWETKIDPPVMN----------ITQVN 170
           |      || ||:| :   |::  ::       : ::|||| |          |:
Db     304 SVIKPTSASYYFRVQAMN--EYNKSCLSK------DVEVDPPVTNEIGPPDVKVDISD-- 353

Qy     171 GSLLVILHAPNLPYRYQKEKNVSIEDYYELLYRVFIINNSL--EKEQKVYEGAHRAVEIE 228
             |:||    |      | :|  | |:  |::    ||   |:| |: |       :
Db     354 ----VLLHIKITPPGGPGNKIMS--DLYDFSYQILYWKNSSDNEEEVKMKETKQTIATVS 407

Qy     229 ALTPHSSYCVVAEIYQPMLDRRSQRSEERCV 259
             | | : |||  : :    :: |  | | |:
Db     408 DLAPSTLYCVKVQAFSEAYNKSSDFSREECI 438


RESULT 13
Q9BUU4
ID   Q9BUU4      PRELIMINARY;      PRT;   325 AA.
AC   Q9BUU4;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Similar to interleukin 10 receptor, beta.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=KIDNEY;
RA   Strausberg R.;
RL   Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC001903; AAH01903.1; -.
DR   HSSP; P13726; 1TFH.
DR   InterPro; IPR000282; Cytok_receptor_2.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR001187; Tissue_factor.
DR   Pfam; PF01108; Tissue_fac; 1.
DR   SMART; SM00060; FN3; 2.
KW   Receptor.
SQ   SEQUENCE   325 AA;  36995 MW;  E470726619AF54C2 CRC64;

  Query Match             10.5%;  Score 149.5;  DB 4;  Length 325;
  Best Local Similarity   24.1%;  Pred. No. 3.4e-06;
  Matches   57;  Conservative   32;  Mismatches   89;  Indels   59;  Gaps    8;

Qy      30 PQRVQFQSRNFHNILQWQPGRALTGN--SSVYFVQYKIMFSCSMKSSHQKPSGCWQHISC 87
           |: |:  | || |||||:      ||    :  :: |:|
Db      24 PENVRMNSVNFKNILQWESPAFAKGNLTFTAQYLSYRIF---------------------- 62

Qy      88 NFPGCRTLAKYGQRQWKNKEDCWGTQELSCDLTSETSDIQEPYYG----RVRAASAGSYS 143
                        :: |  |    || :| :       ||    |||| |  :|
Db      63 -----------------QDKCMNTTLTECDFSSLSK------YGDHTLRVRAEFADEHS 98

Qy     144 EWSMTPRFTPWWETKIDPPVMNITQVNGSLLVILHAPNLPYRYQ--KEKNVSIEDYYELL 201
           :| :   | |  :| | || | :  :  || :   || :   |:    |||    |
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```
Db      99 DW-VNITFCPVDDTIIGPPGMQVEVLADSLHMRFLAPKIENEYETWTMKNV----YNSWT 153

Qy     202 YRVFIINNSLEKEQKVYEGAHRAVEIEALTPHSSYCVVAEIYQPMLDRRSQRSEERC 258
             | |    |  ::: ::       | :  | | ::|||    : |  ::  : ||  |
Db     154 YNVQYWKNGTDEKFQITPQYDFEV-LRNLEPWTTYCVQVRGFLPDRNKAGEWSEPVC 209


RESULT 14
Q8VHM7
ID   Q8VHM7      PRELIMINARY;      PRT;   351 AA.
AC   Q8VHM7;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Interleukin 10 receptor 2 precursor.
GN   IL10R2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RA   Hardy M.P., Hertzog P.J., Owczarek C.M.;
RT   "The genomic structure and expression patterns of the gene encoding
RT   the second chain of the murine interleukin 10 receptor, IL-10R2.";
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF440787; AAL40946.1; -.
DR   InterPro; IPR000282; Cytok_receptor_2.
DR   InterPro; IPR003961; FN_III.
DR   SMART; SM00060; FN3; 2.
KW   Signal; Receptor.
FT   SIGNAL       1     22       POTENTIAL.
SQ   SEQUENCE   351 AA;  40031 MW;  53102D95809AF5D0 CRC64;

  Query Match             10.4%;  Score 149;  DB 11;  Length 351;
  Best Local Similarity   26.7%;  Pred. No. 4.1e-06;
  Matches   71;  Conservative   30;  Mismatches   87;  Indels   78;  Gaps   13;

Qy       8 GFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQ----PGRALTGNSSVYFVQY 63
             |:|  | |     |          |::|:  | || |||||:    |   ||     :  ||
Db       9 GWLGGFLLVPALGMIP-----PPEKVRMNSVNFKNILQWEVPAFPKTNLT-----FTAQY 58

Qy      64 KIMFS----CSMKSSHQKPSGCWQHISCNFPGCRTLAKYGQRQWKNKEDCWGTQELSCDL 119
           :   |     |   :| |          |:|     |:|||
Db      59 ESYRSFQDHCKRTASTQ----------CDF---SHLSKYGD------------------ 86

Qy     120 TSETSDIQEPYYGRVRAASAGSYSEWSMTPRFTPWWETKIDPPVMNITQVNGSLLVILHA 179
                     |  ||||  |  :||| :   | |  :| | || | |  :  || :   |
Db      87 ----------YTVRVRAELADEHSEW-VNVTFCPVEDTIIGPPEMQIESLAESLHLRFSA 135

Qy     180 PNLPYRYQKE------KNVSIEDYYELLYRV-FIINNSLEKEQKVYEGAHRAVEIEALTP 232
           | :    : |      ||:    |    ||| :  | : || | |    : :  :  | |
Db     136 PQI----ENEPETWTLKNI----YDSWAYRVQYWKNGTNEKFQVV--SPYDSEVLRNLEP 185

Qy     233 HSSYCVVAEIYQPMLDRRSQRSEERC 258
             ::||:  : :    :|  : ||  |
Db     186 WTTYCIQVQGFLLDQNRTGEWSEPIC 211


RESULT 15
Q8WTZ2
ID   Q8WTZ2      PRELIMINARY;      PRT;   557 AA.
AC   Q8WTZ2;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Hypothetical 63.5 kDa protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
```

```
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN;
RA   Strausberg R.;
RL   Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC021825; AAH21825.1; -.
DR   InterPro; IPR000282; Cytok_receptor_2.
KW   Hypothetical protein.
SQ   SEQUENCE   557 AA;  63525 MW;  24A01779DB7F356F CRC64;

  Query Match             9.6%;  Score 136.5;  DB 4;  Length 557;
  Best Local Similarity   20.8%;  Pred. No. 0.00012;
  Matches   54;  Conservative   39;  Mismatches  115;  Indels   51;  Gaps    7;

Qy       2 PKHCFLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVYFV 61
           | ||               |   :|   |: ::   :| : :|:|      |  :  : |
Db     217 PVHCI------------KTTVENELPPPENIEVSVQNQNYVLKWD----YTYANMTFQV 259

Qy      62 QYKIMFSCSMKSSHQKPSGCWQHISCNFPGCRTLAKYGQRQWKNKEDCWGTQELSCDLTS 121
           |:   |      :|                          :||   ||   :   |
Db     260 QWLHAFLKRNPGNH-----------------------LYKWKQIPDCENVKTTQCVFPQ 295

Qy     122 ETSDIQEPYYGRVRAASAGSYSEWSMTPRFTPWWETKIDPPVMNITQVNGSLLVILHAPN 181
             :  |  ||:|:   : | ||   :|    :  : ||| ||  :: |  : : ||
Db     296 NVFQ-KGIYLLRVQASDGNNTSFWSEEIKFDTEIQAFLLPPVFNIRSLSDSFHIYIGAP- 353

Qy     182 LPYRYQKEKNVSIEDYYELLYRVFIINNSLEKEQKVYEGAHRAVEIEALTPHSSYCVVAE 241
             ::  |  :   | |:| :    |:   |:|: |     | :  | | : ||| |
Db     354 -----KQSGNTPVIQDYPLIYEIIFWENTSNAERKIIE-KKTDVTVPNLKPLTVYCVKAR 407

Qy     242 IY--QPMLDRRSQRSEERC 258
             :    |:: |  |:  |
Db     408 AHTMDEKLNKSSVFSDAVC 426

Search completed: December 22, 2002, 10:13:19
Job time : 83 secs
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